

SEQUENCE LISTING

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<120> CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
ACID MOLECULES, AND USES THEREOF

<130> IM-2-C2

<140> not yet assigned

<141> 1999-12-01

<150> 09/322,409

<151> 1999-05-28

<150> 60/087,306

<151> 1998-05-29

<160> 174

<170> PatentIn Ver. 2.0

<210> 1

<211> 549

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (43)..(438)

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Ser Gln Leu Ile Pro Thr Leu Val Cys Leu Leu Ala Leu Thr Ser Thr
5 10 15 20

ttt gtc cac gga cat aac ttc aat att act att aaa gag atc atc aaa 150
Phe Val His Gly His Asn Phe Asn Ile Thr Ile Lys Glu Ile Ile Lys
25 30 35

atg ttg aac atc ctc aca gcg aga aac gac tcg tgc atg gag ctg act 198

Met Leu Asn Ile Leu Thr Ala Arg Asn Asp Ser Cys Met Glu Leu Thr
 40 45 50

gtc aag gac gtc ttc act gct cca aag aac aca agc gat aag gaa atc 246
 Val Lys Asp Val Phe Thr Ala Pro Lys Asn Thr Ser Asp Lys Glu Ile
 55 60 65

ttc tgc aga gct gct act gta ctg cgg cag atc tat aca cac aac tgc 294
 Phe Cys Arg Ala Ala Thr Val Leu Arg Gln Ile Tyr Thr His Asn Cys
 70 75 80

tcc aac aga tat ctc aga gga ctc tac agg aac ctc agc agc atg gca 342
 Ser Asn Arg Tyr Leu Arg Gly Leu Tyr Arg Asn Leu Ser Ser Met Ala
 85 90 95 100

aac aag acc tgt tct atg aat gaa atc aag aag agt aca ctg aaa gac 390
 Asn Lys Thr Cys Ser Met Asn Glu Ile Lys Lys Ser Thr Leu Lys Asp
 105 110 115

ttc ttg gaa agg cta aaa gtg atc atg cag aag aaa tac tac agg cat 438
 Phe Leu Glu Arg Leu Lys Val Ile Met Gln Lys Lys Tyr Tyr Arg His
 120 125 130

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atttataaca taataaaata aaatatatat agaaaaaaaa aaaaaaaaaa a 549

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Glu Ile Ile Lys Met Leu Asn Ile Leu Thr Ala Arg Asn Asp Ser Cys
 35 40 45

Met Glu Leu Thr Val Lys Asp Val Phe Thr Ala Pro Lys Asn Thr Ser
 50 55 60

Asp Lys Glu Ile Phe Cys Arg Ala Ala Thr Val Leu Arg Gln Ile Tyr
 65 70 75 80

661027: 434566

Thr His Asn Cys Ser Asn Arg Tyr Leu Arg Gly Leu Tyr Arg Asn Leu
 85 90 95

Ser Ser Met Ala Asn Lys Thr Cys Ser Met Asn Glu Ile Lys Lys Ser
 100 105 110

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Tyr Tyr Arg His
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 gaagatttcc ttatcgcttg tgttctttgg agcagtgaag acgtccttga cagtcagctc 360
 catgcacgag tcgtttctcg ctgtgaggat gttcaacatt ttgatgatct cttaaatagt 420
 aatattgaag ttatgtccgt ggacaaaggt gctggtgagt gctagtaagc agaccagagt 480
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 cctcgtgcc 549

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ctcacagcga gaaacgactc gtgcatggag ctgactgtca aggacgtctt cactgctcca 180
aagaacacaa gcgataagga aatcttctgc agagctgcta ctgtactgcg gcagatctat 240
acacacaact gctccaacag atatctcaga ggactctaca ggaacctcag cagcatggca 300
aacaagacct gttctatgaa tgaaatcaag aagagtacac tgaaagactt cttggaaaag 360
ctaaaagtga tcatgcagaa gaaatactac aggcac 396

<210> 5
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gagtcctctg agatatctgt tggagcagtt gtgtgtatag atctgccgca gtacagtagc 180
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agtcagctcc atgcacgagt cgtttctcgc tgtgaggatg ttcaacattt tgatgatctc 300
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<222> (35)..(916)

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1

5

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Trp Ser Pro Thr Ala Ser Leu Leu Leu Leu Leu Leu Ser Pro Gly	
10 15 20	
ctc cgc ggg acc ccc gac tgc tcc ttc agc cac agc ccc atc tcc tcc	151
Leu Arg Gly Thr Pro Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser	
25 30 35	
acc ttc gcg gtc acc atc cgc aag ctg tct gat tac ctg ctt cag gac	199
Thr Phe Ala Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp	
40 45 50 55	
tat cca gtc act gtc gcc tcc aac ctg cag gac gac gag ctc tgc ggg	247
Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly	
60 65 70	
gcg ttc tgg cgc ctg gtc ctg gcc cag cgc tgg atg gtg cgg ctc cag	295
Ala Phe Trp Arg Leu Val Leu Ala Gln Arg Trp Met Val Arg Leu Gln	
75 80 85	
gct gtg gct gga tcc caa atg caa atc ctg ctg gag gct gtc aac acg	343
Ala Val Ala Gly Ser Gln Met Gln Ile Leu Leu Glu Ala Val Asn Thr	
90 95 100	
gag ata cac ttt gtc acc ttc tgt gcc ttc cag ccc ctc ccc agc tgt	391
Glu Ile His Phe Val Thr Phe Cys Ala Phe Gln Pro Leu Pro Ser Cys	
105 110 115	
ctt cgc ttc gtc cag acc aac atc tcc cac ctc ctg cag gac acc tcc	439
Leu Arg Phe Val Gln Thr Asn Ile Ser His Leu Leu Gln Asp Thr Ser	
120 125 130 135	
cag cag ctg gcc gcc ctg aag ccc tgg atc acc cgc agg aat ttc tcc	487
Gln Gln Leu Ala Ala Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser	
140 145 150	
ggg tgc ctg gag ctg cag tgt cag ccc gac tcc tct aca ttg gtg ccc	535
Gly Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Val Pro	
155 160 165	
cca agg agc ccc ggg gcc ctg gag gcc act gcc ttg cca gcc cct cag	583
Pro Arg Ser Pro Gly Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln	
170 175 180	
gca cct cgg ctg ctc ctc ctg ctg ctg ctg ccc gtg gct ctc ctg ctg	631
Ala Pro Arg Leu Leu Leu Leu Leu Leu Leu Pro Val Ala Leu Leu Leu	
185 190 195	

atg tcc act gcc tgg tgc ctg cat tgg cga agg agg cgg cgg cgg agg 679
 Met Ser Thr Ala Trp Cys Leu His Trp Arg Arg Arg Arg Arg Arg
 200 205 210 215

tca ccc tac cct ggg gag cag agg aca ctg agg ccc agc gag cgg agc 727
 Ser Pro Tyr Pro Gly Glu Gln Arg Thr Leu Arg Pro Ser Glu Arg Ser
 220 225 230

cat ctg ccc gag gac aca gag ctg gga cct gga ggg agt cag cta gag 775
 His Leu Pro Glu Asp Thr Glu Leu Gly Pro Gly Gly Ser Gln Leu Glu
 235 240 245

act ggt ccc ttc ctc gac cac gca gcc ccg ctc gct ccc tcc cca gga 823
 Thr Gly Pro Phe Leu Asp His Ala Ala Pro Leu Ala Pro Ser Pro Gly
 250 255 260

tca agg caa cgc ccg ccc cca acg ccc cca aag cca gcc cca gcc cca 871
 Ser Arg Gln Arg Pro Pro Pro Thr Pro Pro Lys Pro Ala Pro Ala Pro
 265 270 275

cct ctc ccc ctc tgt aca aag tcc ttg ccc cca aga aat tgt ata 916
 Pro Leu Pro Leu Cys Thr Lys Ser Leu Pro Pro Arg Asn Cys Ile
 280 285 290

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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1013

<210> 7
 <211> 294
 <212> PRT
 <213> Canis familiaris

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 20 25 30

Ser His Ser Pro Ile Ser Ser Thr Phe Ala Val Thr Ile Arg Lys Leu
 35 40 45

Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
 50 55 60

<212> DNA

<213> Canis familiaris

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<210> 9

<211> 882

<212> DNA

<213> Canis familiaris

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<210> 10
<211> 882
<212> DNA
<213> Canis familiaris

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cagggccccg gggctccttg ggggcaccaa tgtagaggag tcgggctgac actgcagctc 420

caggcaccgc gagaaattcc tgcgggtgat ccagggttc agggcggcca gctgctggga 480
 ggtgtcctgc aggaggtggg agatgttggt ctggacgaag cgaagacagc tggggagggg 540
 ctggaaggca cagaaggtga caaagtgtat ctccgtgttg acagcctcca gcaggatttg 600
 catttgggat ccagccacag cctggagccg caccatccag cgctgggcca ggaccaggcg 660
 ccagaacgcc ccgcagagct cgtcgtcctg caggttggag gcgacagtga ctggatagtc 720
 ctgaagcagg taatcagaca gcttgccgat ggtgaccgcg aaggtggagg agatggggct 780
 gtggctgaag gagcagtcgg ggggtcccgcg gaggccgggg ctgagcagca gcagcagcaa 840
 cagggaggca gttgggctcc aggtgggcgc cagcactatc at 882

<210> 11
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 Primer

<400> 11
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<210> 12
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 Primer

<400> 12
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<210> 13
 <211> 20
 <212> DNA
 <213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
Primer

<400> 13

ctggcgccag cctggagccc

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<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
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<210> 15

<211> 18

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
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<210> 16

<211> 18

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
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<210> 17

<211> 18
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 <213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
 Primer

<400> 17
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<210> 18
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<223> Description of Artificial Sequence: Synthetic
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<400> 18
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 <212> DNA
 <213> Canis familiaris

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<221> CDS
 <222> (1)..(324)

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ctc aca gcg aga aac gac tcg tgc atg gag ctg act gtc aag gac gtc 96
 Leu Thr Ala Arg Asn Asp Ser Cys Met Glu Leu Thr Val Lys Asp Val
 20 25 30

ttc act gct cca aag aac aca agc gat aag gaa atc ttc tgc aga gct 144
 Phe Thr Ala Pro Lys Asn Thr Ser Asp Lys Glu Ile Phe Cys Arg Ala
 35 40 45

gct act gta ctg cgg cag atc tat aca cac aac tgc tcc aac aga tat 192

Ala Thr Val Leu Arg Gln Ile Tyr Thr His Asn Cys Ser Asn Arg Tyr
50 55 60

ctc aga gga ctc tac agg aac ctc agc agc atg gca aac aag acc tgt 240
Leu Arg Gly Leu Tyr Arg Asn Leu Ser Ser Met Ala Asn Lys Thr Cys
65 70 75 80

tct atg aat gaa atc aag aag agt aca ctg aaa gac ttc ttg gaa agg 288
Ser Met Asn Glu Ile Lys Lys Ser Thr Leu Lys Asp Phe Leu Glu Arg
85 90 95

cta aaa gtg atc atg cag aag aaa tac tac agg cat 324
Leu Lys Val Ile Met Gln Lys Lys Tyr Tyr Arg His
100 105

<210> 20
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<212> PRT
<213> Canis familiaris

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20 25 30

Phe Thr Ala Pro Lys Asn Thr Ser Asp Lys Glu Ile Phe Cys Arg Ala
35 40 45

Ala Thr Val Leu Arg Gln Ile Tyr Thr His Asn Cys Ser Asn Arg Tyr
50 55 60

Leu Arg Gly Leu Tyr Arg Asn Leu Ser Ser Met Ala Asn Lys Thr Cys
65 70 75 80

Ser Met Asn Glu Ile Lys Lys Ser Thr Leu Lys Asp Phe Leu Glu Arg
85 90 95

Leu Lys Val Ile Met Gln Lys Lys Tyr Tyr Arg His
100 105

<210> 21
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<213> Canis familiaris

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 gagtcctctg agatatctgt tggagcagtt gtgtgtatag atctgccgca gtacagtagc 180
 agctctgcag aagatttcct tctcgttctg gttctttgga gcagtgaaga cgtccttgac 240
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<210> 22
 <211> 804
 <212> DNA
 <213> Canis familiaris

<220>
 <221> CDS
 <222> (1)..(804)

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 gtc acc atc cgc aag ctg tct gat tac ctg ctt cag gac tat cca gtc 96
 Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val
 20 25 30
 act gtc gcc tcc aac ctg cag gac gac gag ctc tgc ggg gcg ttc tgg 144
 Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp
 35 40 45
 cgc ctg gtc ctg gcc cag cgc tgg atg gtg cgg ctc cag gct gtg gct 192
 Arg Leu Val Leu Ala Gln Arg Trp Met Val Arg Leu Gln Ala Val Ala
 50 55 60
 gga tcc caa atg caa atc ctg ctg gag gct gtc aac acg gag ata cac 240
 Gly Ser Gln Met Gln Ile Leu Leu Glu Ala Val Asn Thr Glu Ile His
 65 70 75 80
 ttt gtc acc ttc tgt gcc ttc cag ccc ctc ccc agc tgt ctt cgc ttc 288
 Phe Val Thr Phe Cys Ala Phe Gln Pro Leu Pro Ser Cys Leu Arg Phe
 85 90 95

gtc cag acc aac atc tcc cac ctc ctg cag gac acc tcc cag cag ctg	336
Val Gln Thr Asn Ile Ser His Leu Leu Gln Asp Thr Ser Gln Gln Leu	
100 105 110	
gcc gcc ctg aag ccc tgg atc acc cgc agg aat ttc tcc ggg tgc ctg	384
Ala Ala Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu	
115 120 125	
gag ctg cag tgt cag ccc gac tcc tct aca ttg gtg ccc cca agg agc	432
Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Val Pro Pro Arg Ser	
130 135 140	
ccc ggg gcc ctg gag gcc act gcc ttg cca gcc cct cag gca cct cgg	480
Pro Gly Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln Ala Pro Arg	
145 150 155 160	
ctg ctc ctc ctg ctg ctg ctg ccc gtg gct ctc ctg ctg atg tcc act	528
Leu Leu Leu Leu Leu Leu Leu Pro Val Ala Leu Leu Leu Met Ser Thr	
165 170 175	
gcc tgg tgc ctg cat tgg cga agg agg cgg cgg cgg agg tca ccc tac	576
Ala Trp Cys Leu His Trp Arg Arg Arg Arg Arg Arg Arg Ser Pro Tyr	
180 185 190	
cct ggg gag cag agg aca ctg agg ccc agc gag cgg agc cat ctg ccc	624
Pro Gly Glu Gln Arg Thr Leu Arg Pro Ser Glu Arg Ser His Leu Pro	
195 200 205	
gag gac aca gag ctg gga cct gga ggg agt cag cta gag act ggt ccc	672
Glu Asp Thr Glu Leu Gly Pro Gly Gly Ser Gln Leu Glu Thr Gly Pro	
210 215 220	
ttc ctc gac cac gca gcc ccg ctc gct ccc tcc cca gga tca agg caa	720
Phe Leu Asp His Ala Ala Pro Leu Ala Pro Ser Pro Gly Ser Arg Gln	
225 230 235 240	
cgc ccg ccc cca acg ccc cca aag cca gcc cca gcc cca cct ctc ccc	768
Arg Pro Pro Pro Thr Pro Pro Lys Pro Ala Pro Ala Pro Pro Leu Pro	
245 250 255	
ctc tgt aca aag tcc ttg ccc cca aga aat tgt ata	804
Leu Cys Thr Lys Ser Leu Pro Pro Arg Asn Cys Ile	
260 265	

<210> 23
<211> 268

<212> PRT

<213> Canis familiaris

<400> 23

Thr Pro Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser Thr Phe Ala
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20 25 30

Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp
35 40 45

Arg Leu Val Leu Ala Gln Arg Trp Met Val Arg Leu Gln Ala Val Ala
50 55 60

Gly Ser Gln Met Gln Ile Leu Leu Glu Ala Val Asn Thr Glu Ile His
65 70 75 80

Phe Val Thr Phe Cys Ala Phe Gln Pro Leu Pro Ser Cys Leu Arg Phe
85 90 95

Val Gln Thr Asn Ile Ser His Leu Leu Gln Asp Thr Ser Gln Gln Leu
100 105 110

Ala Ala Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu
115 120 125

Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Val Pro Pro Arg Ser
130 135 140

Pro Gly Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln Ala Pro Arg
145 150 155 160

Leu Leu Leu Leu Leu Leu Leu Pro Val Ala Leu Leu Leu Met Ser Thr
165 170 175

Ala Trp Cys Leu His Trp Arg Arg Arg Arg Arg Arg Arg Ser Pro Tyr
180 185 190

Pro Gly Glu Gln Arg Thr Leu Arg Pro Ser Glu Arg Ser His Leu Pro
195 200 205

Glu Asp Thr Glu Leu Gly Pro Gly Gly Ser Gln Leu Glu Thr Gly Pro
210 215 220

Phe Leu Asp His Ala Ala Pro Leu Ala Pro Ser Pro Gly Ser Arg Gln
225 230 235 240

Arg Pro Pro Pro Thr Pro Pro Lys Pro Ala Pro Ala Pro Pro Leu Pro
 245 250 255

Leu Cys Thr Lys Ser Leu Pro Pro Arg Asn Cys Ile
 260 265

<210> 24
 <211> 804
 <212> DNA
 <213> Canis familiaris

<400> 24
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 gtggtcgagg aagggaccag tctctagctg actccctcca ggtcccagct ctgtgtcctc 180
 gggcagatgg ctccgctcgc tgggcctcag tgtcctctgc tccccagggg aggggtgacct 240
 ccgcgcgcgc ctcccttcgcc aatgcaggca ccaggcagtg gacatcagca ggagagccac 300
 gggcagcagc agcaggagga gcagccgagg tgcctgaggg gctggcaagg cagtggcctc 360
 cagggccccg gggctccttg ggggcaccaa tgtagaggag tcgggctgac actgcagctc 420
 caggcacccg gagaaattcc tgcgggtgat ccagggttc agggcggcca gctgctggga 480
 ggtgtcctgc aggaggtggg agatgttggg ctggacgaag cgaagacagc tggggagggg 540
 ctggaaggca cagaaggtga caaagtgtat ctccgtgttg acagcctcca gcaggatttg 600
 catttgggat ccagccacag cctggagccg caccatccag cgctgggcca ggaccaggcg 660
 ccagaacgcc ccgcagagct cgtcgtcctg caggttggag gcgacagtga ctggatagtc 720
 ctgaagcagg taatcagaca gcttgccgat ggtgaccgcg aaggtggagg agatggggct 780
 gtggctgaag gagcagtcgg gggt 804

<210> 25
 <211> 985
 <212> DNA
 <213> Canis familiaris

<220>

<221> CDS

<222> (74)..(901)

<400> 25

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gcctccggcc gag atg ata gtg ctg gcg cca gcc tgg agc cca act gcc 109

Met Ile Val Leu Ala Pro Ala Trp Ser Pro Thr Ala

1

5

10

tcc ctg ttg ctg ctg ctg ctg ctc agc ccc ggc ctc cgc ggg acc ccc 157

Ser Leu Leu Leu Leu Leu Leu Leu Ser Pro Gly Leu Arg Gly Thr Pro

15

20

25

gac tgc tcc ttc agc cac agc ccc atc tcc tcc acc ttc gcg gtc acc 205

Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser Thr Phe Ala Val Thr

30

35

40

atc cgc aag ctg tct gat tac ctg ctt cag gac tat cca gtc act gtc 253

Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val

45

50

55

60

gcc tcc aac ctg cag gac gac gag ctc tgc ggg gcg ttc tgg cgc ctg 301

Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp Arg Leu

65

70

75

gtc ctg gcc cag cgc tgg atg gtg cgg ctc cag gct gtg gct gga tcc 349

Val Leu Ala Gln Arg Trp Met Val Arg Leu Gln Ala Val Ala Gly Ser

80

85

90

caa atg caa atc ctg ctg gag gct gtc aac acg gag ata cac ttt gtc 397

Gln Met Gln Ile Leu Leu Glu Ala Val Asn Thr Glu Ile His Phe Val

95

100

105

acc ttc tgt gcc ttc cag gac acc tcc cag cag ctg gcc gcc ctg aag 445

Thr Phe Cys Ala Phe Gln Asp Thr Ser Gln Gln Leu Ala Ala Leu Lys

110

115

120

ccc tgg atc acc cgc agg aat ttc tcc ggg tgc ctg gag ctg cag tgt 493

Pro Trp Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu Glu Leu Gln Cys

125

130

135

140

cag ccc gac tcc tct aca ttg gtg ccc cca agg agc ccc ggg gcc ctg 541

Gln Pro Asp Ser Ser Thr Leu Val Pro Pro Arg Ser Pro Gly Ala Leu

145

150

155

gag gcc act gcc ttg cca gcc cct cag gca cct cgg ctg ctc ctc ctg 589

Glu Ala Thr Ala Leu Pro Ala Pro Gln Ala Pro Arg Leu Leu Leu Leu
 160 165 170

ctg ctg ctg ccc gtg gct ctc ctg ctg atg tcc act gcc tgg tgc ctg 637
 Leu Leu Leu Pro Val Ala Leu Leu Leu Met Ser Thr Ala Trp Cys Leu
 175 180 185

cat tgg cga agg agg cgg cgg cgg agg tca ccc tac cct ggg gag cag 685
 His Trp Arg Arg Arg Arg Arg Arg Arg Ser Pro Tyr Pro Gly Glu Gln
 190 195 200

agg aca ctg agg ccc agc gag cgg agc cat ctg ccc gag gac aca gag 733
 Arg Thr Leu Arg Pro Ser Glu Arg Ser His Leu Pro Glu Asp Thr Glu
 205 210 215 220

ctg gga cct gga ggg agt cag cta gag act ggt ccc ttc ctc gac cac 781
 Leu Gly Pro Gly Gly Ser Gln Leu Glu Thr Gly Pro Phe Leu Asp His
 225 230 235

gca gcc ccg ctc gct ccc tcc cca gga tca agg caa cgc ccg ccc cca 829
 Ala Ala Pro Leu Ala Pro Ser Pro Gly Ser Arg Gln Arg Pro Pro Pro
 240 245 250

acg ccc cca aag cca gcc cca gcc cca cct ctc ccc ctc tgt aca aag 877
 Thr Pro Pro Lys Pro Ala Pro Ala Pro Pro Leu Pro Leu Cys Thr Lys
 255 260 265

tcc ttg ccc cca aga aat tgt ata taaatcatcc ttttctacca gcaaaaaaaaa 931
 Ser Leu Pro Pro Arg Asn Cys Ile
 270 275

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 985

<210> 26
 <211> 276
 <212> PRT
 <213> Canis familiaris

<400> 26
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 Leu Leu Leu Leu Ser Pro Gly Leu Arg Gly Thr Pro Asp Cys Ser Phe
 20 25 30
 Ser His Ser Pro Ile Ser Ser Thr Phe Ala Val Thr Ile Arg Lys Leu
 35 40 45

Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
50 55 60

Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp Arg Leu Val Leu Ala Gln
65 70 75 80

Arg Trp Met Val Arg Leu Gln Ala Val Ala Gly Ser Gln Met Gln Ile
85 90 95

Leu Leu Glu Ala Val Asn Thr Glu Ile His Phe Val Thr Phe Cys Ala
100 105 110

Phe Gln Asp Thr Ser Gln Gln Leu Ala Ala Leu Lys Pro Trp Ile Thr
115 120 125

Arg Arg Asn Phe Ser Gly Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser
130 135 140

Ser Thr Leu Val Pro Pro Arg Ser Pro Gly Ala Leu Glu Ala Thr Ala
145 150 155 160

Leu Pro Ala Pro Gln Ala Pro Arg Leu Leu Leu Leu Leu Leu Pro
165 170 175

Val Ala Leu Leu Leu Met Ser Thr Ala Trp Cys Leu His Trp Arg Arg
180 185 190

Arg Arg Arg Arg Arg Ser Pro Tyr Pro Gly Glu Gln Arg Thr Leu Arg
195 200 205

Pro Ser Glu Arg Ser His Leu Pro Glu Asp Thr Glu Leu Gly Pro Gly
210 215 220

Gly Ser Gln Leu Glu Thr Gly Pro Phe Leu Asp His Ala Ala Pro Leu
225 230 235 240

Ala Pro Ser Pro Gly Ser Arg Gln Arg Pro Pro Pro Thr Pro Pro Lys
245 250 255

Pro Ala Pro Ala Pro Pro Leu Pro Leu Cys Thr Lys Ser Leu Pro Pro
260 265 270

Arg Asn Cys Ile
275

<210> 27

<211> 985
<212> DNA
<213> Canis familiaris

<400> 27

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tggggagggg gcgagcgggg ctgcgtggtc gaggaaggga ccagtctcta gctgactccc 240
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ggagtcgggc tgacactgca gctccaggca cccggagaaa ttcctgcggg tgatccaggg 540
cttcagggcg gccagctgct gggaggtgtc ctggaaggca cagaagggtga caaagtgtat 600
ctcgtgttg acagcctcca gcaggatttg catttgggat ccagccacag cctggagccg 660
caccatccag cgctgggcca ggaccaggcg ccagaacgcc ccgcagagct cgtcgtcctg 720
caggttgag gcgacagtga ctggatagtc ctgaagcagg taatcagaca gcttgcgat 780
ggtgaccgag aaggtggagg agatggggct gtggctgaag gagcagtcgg gggccccgag 840
gaggccgggg ctgagcagca gcagcagcaa cagggaggca gttgggctcc aggctggcgc 900
cagcactatc atctcggccg gagggccctc atgcctatgg tcagatcagg cttgccccag 960
ctgggcgtgg aaggggccag gccgg 985

<210> 28
<211> 828
<212> DNA
<213> Canis familiaris

<400> 28

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agccccggcc tccgcgggac ccccgactgc tccttcagcc acagccccat ctcctccacc 120
 ttcgcggtca ccatccgcaa gctgtctgat tacctgcttc aggactatcc agtcactgtc 180
 gcctccaacc tgcaggacga cgagctctgc gggcggttct ggcgctggt cctggcccag 240
 cgctggatgg tgcggctcca ggctgtggct ggatcccaaa tgcaaatacct gctggaggct 300
 gtcaacacgg agatacactt tgtcaccttc tgtgccttcc aggacacctc ccagcagctg 360
 gccgccctga agccctggat caccgcgagg aatttctccg ggtgcctgga gctgcagtgt 420
 cagcccgact cctctacatt ggtgccccca aggagccccg gggccctgga ggccactgcc 480
 ttgccagccc ctcaggcacc tcggctgctc ctcctgctgc tgctgcccgt ggctctctctg 540
 ctgatgtcca ctgcctgggtg cctgcattgg cgaaggaggc ggcggcggag gtcaccctac 600
 cctgggggagc agaggacact gagggcccagc gagcggagcc atctgcccga ggacacagag 660
 ctgggacctg gagggagtca gctagagact ggtcccttcc tcgaccacgc agccccgctc 720
 gctccctccc caggatcaag gcaacgcccg cccccaacgc ccccaaagcc agccccagcc 780
 ccacctctcc ccctctgtac aaagtccttg cccccaagaa attgtata 828

<210> 29
 <211> 828
 <212> DNA
 <213> Canis familiaris

<400> 29
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 gtggctcagg aagggaccag tctctagctg actccctcca ggtcccagct ctgtgtcttc 180
 gggcagatgg ctccgctcgc tgggcctcag tgtcctctgc tcccagggt agggtgacct 240
 ccgccgccgc ctcttcgcc aatgcaggca ccaggcagtg gacatcagca ggagagccac 300
 gggcagcagc agcaggagga gcagccgagg tgcctgaggg gctggcaagg cagtggcctc 360
 caggggccccg gggctccttg ggggcaccaa thtagaggag tcgggctgac actgcagctc 420
 caggcaccgc gagaaattcc tgcgggtgat ccagggcttc agggcgcca gctgctggga 480

ggtgtcctgg aaggcacaga aggtgacaaa gtgtatctcc gtgttgacag cctccagcag 540
 gatttgcatt tgggatccag ccacagcctg gagccgcacc atccagcgct gggccaggac 600
 caggcgccag aacgccccgc agagctcgtc gtccctgcagg ttggaggcga cagtgactgg 660
 atagtcctga agcaggtaat cagacagctt gcggatggtg accgcgaagg tggaggagat 720
 ggggctgtgg ctgaaggagc agtcgggggt cccgcggagg ccggggctga gcagcagcag 780
 cagcaacagg gaggcagttg ggctccaggc tggcgccagc actatcat 828

<210> 30
 <211> 750
 <212> DNA
 <213> Canis familiaris

<220>
 <221> CDS
 <222> (1)..(750)

<400> 30
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 Thr Pro Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser Thr Phe Ala
 1 5 10 15
 gtc acc atc cgc aag ctg tct gat tac ctg ctt cag gac tat cca gtc 96
 Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val
 20 25 30
 act gtc gcc tcc aac ctg cag gac gac gag ctc tgc ggg gcg ttc tgg 144
 Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp
 35 40 45
 cgc ctg gtc ctg gcc cag cgc tgg atg gtg cgg ctc cag gct gtg gct 192
 Arg Leu Val Leu Ala Gln Arg Trp Met Val Arg Leu Gln Ala Val Ala
 50 55 60
 gga tcc caa atg caa atc ctg ctg gag gct gtc aac acg gag ata cac 240
 Gly Ser Gln Met Gln Ile Leu Leu Glu Ala Val Asn Thr Glu Ile His
 65 70 75 80
 ttt gtc acc ttc tgt gcc ttc cag gac acc tcc cag cag ctg gcc gcc 288
 Phe Val Thr Phe Cys Ala Phe Gln Asp Thr Ser Gln Gln Leu Ala Ala
 85 90 95

BBT-2000

1	5	10	15
Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val	20	25	30
Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp	35	40	45
Arg Leu Val Leu Ala Gln Arg Trp Met Val Arg Leu Gln Ala Val Ala	50	55	60
Gly Ser Gln Met Gln Ile Leu Leu Glu Ala Val Asn Thr Glu Ile His	65	70	75
Phe Val Thr Phe Cys Ala Phe Gln Asp Thr Ser Gln Gln Leu Ala Ala	85	90	95
Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu Glu Leu	100	105	110
Gln Cys Gln Pro Asp Ser Ser Thr Leu Val Pro Pro Arg Ser Pro Gly	115	120	125
Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln Ala Pro Arg Leu Leu	130	135	140
Leu Leu Leu Leu Leu Pro Val Ala Leu Leu Leu Met Ser Thr Ala Trp	145	150	155
Cys Leu His Trp Arg Arg Arg Arg Arg Arg Ser Pro Tyr Pro Gly	165	170	175
Glu Gln Arg Thr Leu Arg Pro Ser Glu Arg Ser His Leu Pro Glu Asp	180	185	190
Thr Glu Leu Gly Pro Gly Gly Ser Gln Leu Glu Thr Gly Pro Phe Leu	195	200	205
Asp His Ala Ala Pro Leu Ala Pro Ser Pro Gly Ser Arg Gln Arg Pro	210	215	220
Pro Pro Thr Pro Pro Lys Pro Ala Pro Ala Pro Pro Leu Pro Leu Cys	225	230	235
Thr Lys Ser Leu Pro Pro Arg Asn Cys Ile	245	250	

<210> 32
 <211> 750
 <212> DNA
 <213> Canis familiaris

<400> 32
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 gtggtcgagg aagggaaccag tctctagctg actccctcca ggtcccagct ctgtgtcctc 180
 gggcagatgg ctccgctcgc tgggcctcag tgcctctgc tcccagggg agggtgacct 240
 ccgccgccgc ctcttcgcc aatgcaggca ccaggcagtg gacatcagca ggagagccac 300
 gggcagcagc agcaggagga gcagccgagg tgcctgaggg gctggcaagg cagtggcctc 360
 cagggccccg gggctccttg ggggcaccaa tgtagaggag tcgggctgac actgcagctc 420
 caggcaccgc gagaaattcc tgcgggtgat ccagggcttc agggcggcca gctgctggga 480
 ggtgtcctgg aaggcacaga aggtgacaaa gtgtatctcc gtgttgacag cctccagcag 540
 gatttgcat tgggatccag ccacagcctg gagccgcacc atccagcgct gggccaggac 600
 caggcgccag aacgccccgc agagctcgtc gtcctgcagg ttggaggcga cagtgactgg 660
 atagtctga agcaggtaat cagacagctt gcggatggtg accgcgaagg tggaggagat 720
 ggggctgtgg ctgaaggagc agtcgggggt 750

<210> 33
 <211> 1019
 <212> DNA
 <213> Canis familiaris

<220>
 <221> CDS
 <222> (74)..(166)

<400> 33
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 gcctccggcc gag atg ata gtg ctg gcg cca gcc tgg agc cca act gtg 109
 Met Ile Val Leu Ala Pro Ala Trp Ser Pro Thr Val
 1 5 10

1960

cgt ata ccc ggg gga caa ggc ggg gga cag gca gag cgc tac cga gct 157
 Arg Ile Pro Gly Gly Gln Gly Gly Gly Gln Ala Glu Arg Tyr Arg Ala
 15 20 25

ggg cag agc tgagagagca gacggacaga ggccctccctg ttgctgctgc 206
 Gly Gln Ser
 30

tgctgctcag ccccggcctc cgcgggaccc ccgactgctc cttcagccac agccccatct 266

cctccacctt cgcggtcacc atccgcaagc tgtctgatta cctgcttcag gactatccag 326

tcactgtcgc ctccaacctg caggacgacg agctctgcgg ggcgttcttg cgcctggtcc 386

tggcccagcg ctggatggtg cggctccagg ctgtggctgg atcccaaagt caaatcctgc 446

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ccactgcctt gccagccctt caggcacctc ggctgctcct cctgctgctg ctgcccgtgg 686

ctctcctgct gatgtccact gcctggtgcc tgcattggcg aaggaggcgg cggcggagggt 746

cacctaccc tggggagcag aggacactga ggcccagcga gcggagccat ctgcccgagg 806

acacagagct gggacctgga gggagtcagc tagagactgg tcccttcctc gaccacgcag 866

ccccgctcgc tccctcccca ggatcaaggc aacgcccgcc cccaacgccc ccaaagccag 926

ccccagcccc acctctcccc ctctgtacaa agtccttgcc cccaagaaat tgtatataaa 986

tcctcctttt ctaccaaaaa aaaaaaaaaa aaa 1019

<210> 34

<211> 31

<212> PRT

<213> Canis familiaris

<400> 34

Met Ile Val Leu Ala Pro Ala Trp Ser Pro Thr Val Arg Ile Pro Gly
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Gly Gln Gly Gly Gly Gln Ala Glu Arg Tyr Arg Ala Gly Gln Ser

CGT ATA CCC GGG GGA CAA GGC GGG GGA CAG GCA GAG CGC TAC CGA GCT

<210> 35
 <211> 1019
 <212> DNA
 <213> Canis familiaris

<400> 35
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 gttgccttga tcctggggag ggagcgagcg gggctgcgtg gtcgaggaag ggaccagtct 180
 ctagctgact cctccaggt ccagctctg tgcctcggg cagatggctc cgctcgctgg 240
 gcctcagtgt cctctgtcc ccagggtagg gtgacctcg ccgccgcctc ctctgccaat 300
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 gccgaggtgc ctgaggggct ggcaaggcag tggcctccag ggccccgggg ctcttgggg 420
 gcaccaatgt agaggagtcg ggctgacact gcagctccag gcacccggag aaattcctgc 480
 gggatgatcca gggcttcagg gcggccagct gctgggaggt gtcctggaag gcacagaagg 540
 tgacaaagtg tatctccgtg ttgacagcct ccagcaggat ttgcatttgg gatccagcca 600
 cagcctggag ccgcaccatc cagcgtggg ccaggaccag gcgccagaac gccccgcaga 660
 gctcgtcgtc ctgcaggttg gaggcgacag tgactggata gtcctgaagc aggtaatcag 720
 acagcttgcg gatggtgacc gcgaagggtg aggagatggg gctgtggctg aaggagcagt 780
 cgggggtccc gcggaggccg gggctgagca gcagcagcag caacaggag gctctgtcc 840
 gtctgtcttc tcagctctgc ccagctcggg agcgtctctg ctgtcccccg ccttgcccc 900
 cgggtatacg cacagttggg ctccaggctg gcgccagcac tatcatctcg gccggaggcc 960
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<210> 36
 <211> 93
 <212> DNA
 <213> Canis familiaris

<400> 36
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 ggacaggcag agcgctaccg agctgggcag agc 93

<210> 37
 <211> 93
 <212> DNA
 <213> Canis familiaris

<400> 37
 gctctgccca gctcggtage gctctgctg tccccgcct tgtcccccg gtatacgcac 60
 agttgggctc caggctggcg ccagcactat cat 93

<210> 38
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 Primer

<400> 38
 tgaattcgga cataacttca atattac 27

<210> 39
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 Primer

<400> 39
 tctcgagatt cagcttcaat gcctgta 27

<210> 40
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 40

cccaagctta tgggtctcac ctcccaac

28

<210> 41

<211> 395

<212> DNA

<213> Felis catus

<400> 41

ggccataggc atgaagggcc tccggccgag atgatagtgc tggcgccagc ctggagccca 60

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tccttcagcc acagccccat ctctccacc ttcaagggtca ccatccgaaa gctgtctgat 180

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tgtgccttcc agcccctccc cagctgtctt cgatt

395

<210> 42

<211> 793

<212> DNA

<213> Felis catus

<400> 42

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cgctccaac ctacaggacg acgagctctg tgggccattc tggcacctgg tcctggccca 120

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cttgaagccc tggatcaccg gcaggaatTT ctgggggtgc ctggagctac agtgtcagcc 360

cgactcctcc accccactgc ccccaaggag cccaggggcc ttggaggcca cagccctgcc 420
agccctcag gcccctctgc tgctcctcct gctgctgttg cctgtggctc tcttgctgat 480
gtccgccgcc tgggtgcctgc actggcgaag aaggagatgg agaacgccct accccagggg 540
gcagaggaag aactgaggc ccagagagag gaatcacctg cccgaggaca cagagccggg 600
actcggagaa agtcagctag agactggttc cttcctcgac cacgctgccc cgctcactct 660
ccccccggga tggaggcaac gccagcccc aacgccagcc ccagaccac ctatccccct 720
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aaaaaaaaa aaa 793

<210> 43
<211> 942
<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (31)..(903)

<400> 43
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Met Ile Val Leu Ala Pro Ala Trp
1 5
agc cca act acc tcc ctg ctg ctg ctg cta ctg ctc agc cct ggc ctc 102
Ser Pro Thr Thr Ser Leu Leu Leu Leu Leu Leu Ser Pro Gly Leu
10 15 20
cgc ggg tcc ccc gac tgt tcc ttc agc cac agc ccc atc tcc tcc acc 150
Arg Gly Ser Pro Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser Thr
25 30 35 40
ttc aag gtc acc atc cga aag ctg tct gat tac ctg ctt cag gat tac 198
Phe Lys Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr
45 50 55
cca gtc acc gtc gcc tcc aac cta cag gac gac gag ctc tgt ggg cca 246
Pro Val Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Pro
60 65 70
ttc tgg cac ctg gtc ctg gcc cag cgc tgg atg ggt cgg ctc aag gct 294

Phe Trp His Leu Val Leu Ala Gln Arg Trp Met Gly Arg Leu Lys Ala
 75 80 85

gtg gct ggg tcc cag atg caa agc ctg ctg gag gcg gtc aac acc gag 342
 Val Ala Gly Ser Gln Met Gln Ser Leu Leu Glu Ala Val Asn Thr Glu
 90 95 100

ata cat ttt gtc acc ttg tgt gcc ttc cag ccc ctc ccc agc tgt ctt 390
 Ile His Phe Val Thr Leu Cys Ala Phe Gln Pro Leu Pro Ser Cys Leu
 105 110 115 120

cga ttc gtc cag acc aac atc tcc cac ctc ctg cag gac acc tcc gag 438
 Arg Phe Val Gln Thr Asn Ile Ser His Leu Leu Gln Asp Thr Ser Glu
 125 130 135

cag ctg gcg gcc ttg aag ccc tgg atc acc cgc agg aat ttc tcg ggg 486
 Gln Leu Ala Ala Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser Gly
 140 145 150

tgc ctg gag cta cag tgt cag ccc gac tcc tcc acc cca ctg ccc cca 534
 Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Pro Leu Pro Pro
 155 160 165

agg agc ccc agg gcc ttg gag gcc aca gcc ctg cca gcc cct cag gcc 582
 Arg Ser Pro Arg Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln Ala
 170 175 180

cct ctg ctg ctc ctc ctg ctg ctg ttg cct gtg gct ctc ttg ctg atg 630
 Pro Leu Leu Leu Leu Leu Leu Leu Leu Pro Val Ala Leu Leu Leu Met
 185 190 195 200

tcc gcc gcc tgg tgc ctg cac tgg cga aga agg aga tgg aga acg ccc 678
 Ser Ala Ala Trp Cys Leu His Trp Arg Arg Arg Arg Trp Arg Thr Pro
 205 210 215

tac ccc agg gag cag agg aag aca ctg agg ccc aga gag agg aat cac 726
 Tyr Pro Arg Glu Gln Arg Lys Thr Leu Arg Pro Arg Glu Arg Asn His
 220 225 230

ctg ccc gag gac aca gag ccg gga ctc gga gaa agt cag cta gag act 774
 Leu Pro Glu Asp Thr Glu Pro Gly Leu Gly Glu Ser Gln Leu Glu Thr
 235 240 245

ggc tcc ttc ctc gac cac gct gcc ccg ctc act ctc ccc ccg gga tgg 822
 Gly Ser Phe Leu Asp His Ala Ala Pro Leu Thr Leu Pro Pro Gly Trp
 250 255 260

agg caa cgc cag ccc cca acg cca gcc cca gac cca cct atc ccc ctc 870

Arg Gln Arg Gln Pro Pro Thr Pro Ala Pro Asp Pro Pro Ile Pro Leu
265 270 275 280

tgt aca aag tcc ttg tcc tca gga aat tgt ata taaatcatcc ttttctacca 923
Cys Thr Lys Ser Leu Ser Ser Gly Asn Cys Ile
285 290

aaaaaaaaa aaaaaaaaaa 942

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<212> PRT
<213> Felis catus

<400> 44
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Ser His Ser Pro Ile Ser Ser Thr Phe Lys Val Thr Ile Arg Lys Leu
35 40 45

Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
50 55 60

Gln Asp Asp Glu Leu Cys Gly Pro Phe Trp His Leu Val Leu Ala Gln
65 70 75 80

Arg Trp Met Gly Arg Leu Lys Ala Val Ala Gly Ser Gln Met Gln Ser
85 90 95

Leu Leu Glu Ala Val Asn Thr Glu Ile His Phe Val Thr Leu Cys Ala
100 105 110

Phe Gln Pro Leu Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
115 120 125

His Leu Leu Gln Asp Thr Ser Glu Gln Leu Ala Ala Leu Lys Pro Trp
130 135 140

Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu Glu Leu Gln Cys Gln Pro
145 150 155 160

Asp Ser Ser Thr Pro Leu Pro Pro Arg Ser Pro Arg Ala Leu Glu Ala
165 170 175

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<213> Felis catus

<400> 46
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cagaggaaga cactgaggcc cagagagagg aatcacctgc ccgaggacac agagccggga 720
ctcggagaaa gtcagctaga gactggttcc ttcctcgacc acgctgccc gctcactctc 780

205

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cccccgggat ggaggcaacg ccagcccccacg ccagccagccc cagacccacc tatccccctc 840
 tgtacaaagt ccttgctcctc aggaaattgt ata 873

<210> 47
 <211> 873
 <212> DNA
 <213> Felis catus

<400> 47
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 gaaggaacca gtctctagct gactttctcc gagtcccggc tctgtgtcct cgggcaggtg 180
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 cccacagagc tcgtcgtcct gtaggttggg ggcgacggtg actgggtaat cctgaagcag 720
 gtaatcagac agctttcgga tggtgacctt gaaggtggag gagatggggc tgtggctgaa 780
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<220>

<221> CDS

<222> (1)..(795)

<400> 48

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gtc	acc	atc	cga	aag	ctg	tct	gat	tac	ctg	ctt	cag	gat	tac	cca	gtc	96
Val	Thr	Ile	Arg	Lys	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	
			20					25					30			

acc	gtc	gcc	tcc	aac	cta	cag	gac	gac	gag	ctc	tgt	ggg	cca	ttc	tgg	144
Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Asp	Glu	Leu	Cys	Gly	Pro	Phe	Trp	
			35				40					45				

cac	ctg	gtc	ctg	gcc	cag	cgc	tgg	atg	ggc	cgg	ctc	aag	gct	gtg	gct	192
His	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Gly	Arg	Leu	Lys	Ala	Val	Ala	
	50					55					60					

ggg	tcc	cag	atg	caa	agc	ctg	ctg	gag	gcg	gtc	aac	acc	gag	ata	cat	240
Gly	Ser	Gln	Met	Gln	Ser	Leu	Leu	Glu	Ala	Val	Asn	Thr	Glu	Ile	His	
65				70				75						80		

ttt	gtc	acc	ttg	tgt	gcc	ttc	cag	ccc	ctc	ccc	agc	tgt	ctt	cga	ttc	288
Phe	Val	Thr	Leu	Cys	Ala	Phe	Gln	Pro	Leu	Pro	Ser	Cys	Leu	Arg	Phe	
				85				90						95		

gtc	cag	acc	aac	atc	tcc	cac	ctc	ctg	cag	gac	acc	tcc	gag	cag	ctg	336
Val	Gln	Thr	Asn	Ile	Ser	His	Leu	Leu	Gln	Asp	Thr	Ser	Glu	Gln	Leu	
			100					105					110			

gcg	gcc	ttg	aag	ccc	tgg	atc	acc	cgc	agg	aat	ttc	tcg	ggg	tgc	ctg	384
Ala	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Arg	Asn	Phe	Ser	Gly	Cys	Leu	
		115					120					125				

gag	cta	cag	tgt	cag	ccc	gac	tcc	tcc	acc	cca	ctg	ccc	cca	agg	agc	432
Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Pro	Leu	Pro	Pro	Arg	Ser	
	130					135					140					

ccc	agg	gcc	ttg	gag	gcc	aca	gcc	ctg	cca	gcc	cct	cag	gcc	cct	ctg	480
Pro	Arg	Ala	Leu	Glu	Ala	Thr	Ala	Leu	Pro	Ala	Pro	Gln	Ala	Pro	Leu	
145				150				155						160		

ctg	ctc	ctc	ctg	ctg	ctg	ttg	cct	gtg	gct	ctc	ttg	ctg	atg	tcc	gcc	528
Leu	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Val	Ala	Leu	Leu	Leu	Met	Ser	Ala	
				165				170						175		

gcc tgg tgc ctg cac tgg cga aga agg aga tgg aga acg ccc tac ccc 576
Ala Trp Cys Leu His Trp Arg Arg Arg Arg Trp Arg Thr Pro Tyr Pro
180 185 190

agg gag cag agg aag aca ctg agg ccc aga gag agg aat cac ctg ccc 624
Arg Glu Gln Arg Lys Thr Leu Arg Pro Arg Glu Arg Asn His Leu Pro
195 200 205

gag gac aca gag ccg gga ctc gga gaa agt cag cta gag act ggt tcc 672
Glu Asp Thr Glu Pro Gly Leu Gly Glu Ser Gln Leu Glu Thr Gly Ser
210 215 220

ttc ctc gac cac gct gcc ccg ctc act ctc ccc ccg gga tgg agg caa 720
Phe Leu Asp His Ala Ala Pro Leu Thr Leu Pro Pro Gly Trp Arg Gln
225 230 235 240

cgc cag ccc cca acg cca gcc cca gac cca cct atc ccc ctc tgt aca 768
Arg Gln Pro Pro Thr Pro Ala Pro Asp Pro Pro Ile Pro Leu Cys Thr
245 250 255

aag tcc ttg tcc tca gga aat tgt ata 795
Lys Ser Leu Ser Ser Gly Asn Cys Ile
260 265

<210> 49
<211> 265
<212> PRT
<213> Felis catus

<400> 49
Ser Pro Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser Thr Phe Lys
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Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val
20 25 30

Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Pro Phe Trp
35 40 45

His Leu Val Leu Ala Gln Arg Trp Met Gly Arg Leu Lys Ala Val Ala
50 55 60

Gly Ser Gln Met Gln Ser Leu Leu Glu Ala Val Asn Thr Glu Ile His
65 70 75 80

Phe Val Thr Leu Cys Ala Phe Gln Pro Leu Pro Ser Cys Leu Arg Phe

85

90

95

Val Gln Thr Asn Ile Ser His Leu Leu Gln Asp Thr Ser Glu Gln Leu
100 105 110

Ala Ala Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu
115 120 125

Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Pro Leu Pro Pro Arg Ser
130 135 140

Pro Arg Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln Ala Pro Leu
145 150 155 160

Leu Leu Leu Leu Leu Leu Leu Pro Val Ala Leu Leu Leu Met Ser Ala
165 170 175

Ala Trp Cys Leu His Trp Arg Arg Arg Arg Trp Arg Thr Pro Tyr Pro
180 185 190

Arg Glu Gln Arg Lys Thr Leu Arg Pro Arg Glu Arg Asn His Leu Pro
195 200 205

Glu Asp Thr Glu Pro Gly Leu Gly Glu Ser Gln Leu Glu Thr Gly Ser
210 215 220

Phe Leu Asp His Ala Ala Pro Leu Thr Leu Pro Pro Gly Trp Arg Gln
225 230 235 240

Arg Gln Pro Pro Thr Pro Ala Pro Asp Pro Pro Ile Pro Leu Cys Thr
245 250 255

Lys Ser Leu Ser Ser Gly Asn Cys Ile
260 265

<210> 50

<211> 795

<212> DNA

<213> Felis catus

<400> 50

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gaaggaacca gtctctagct gactttctcc gactcccggc tctgtgtcct cgggcaggtg 180

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 ccttcttcgc cagtgcaggc accaggcggc ggacatcagc aagagagcca caggcaacag 300
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 ggggctcctt gggggcagtg ggggtggagga gtcgggctga cactgtagct ccaggcaccc 420
 cgagaaattc ctgcgggtga tccagggtt caaggccgcc agctgctcgg aggtgtcctg 480
 caggaggtgg gagatgttgg tctggacgaa tcgaagacag ctggggaggg gctggaaggc 540
 acacaaggtg acaaaatgta tctcgggtgt gaccgcctcc agcaggcttt gcatctggga 600
 cccagccaca gccttgagcc gacccatcca gcgctgggcc aggaccaggt gccagaatgg 660
 cccacagagc tcgtcgtcct gtaggttga ggcgacggtg actgggtaat cctgaagcag 720
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 ggaacagtcg gggga 795

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 <213> Canis familiaris

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 agagccctag tgggtggtccc catcattatg gggatcctgc ttgttgcct gttggtgtct 180
 gcctgcatcc gaaagggtgt caagaagcca gagaataagg ttatgtatca ggaccctgtg 240
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 <212> DNA
 <213> Canis familiaris

<220>

<221> CDS

<222> (196)..(1017)

<400> 52

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gggcgggggc aagggtctggg gagttactaa agacatcccc gcgcccctac tccgctgcct 180

gctattcacc tcgcc atg gtt ctc ctg cct ctg cgc tgt ctc ttc tgg ggc 231

Met Val Leu Leu Pro Leu Arg Cys Leu Phe Trp Gly

1

5

10

tcc ttg ttg acc acc gtc tac cca gaa cca cgc act gca tgc aga gaa 279

Ser Leu Leu Thr Thr Val Tyr Pro Glu Pro Arg Thr Ala Cys Arg Glu

15

20

25

aag caa tac cta gta gac agt cag tgc tgt aat atg tgc cca cca gga 327

Lys Gln Tyr Leu Val Asp Ser Gln Cys Cys Asn Met Cys Pro Pro Gly

30

35

40

gag aaa ctg gtg aat gac tgc cta cat acc att gac acg gaa tgc act 375

Glu Lys Leu Val Asn Asp Cys Leu His Thr Ile Asp Thr Glu Cys Thr

45

50

55

60

cgt tgc caa aca ggc gaa ttc cta gac act tgg aac gca gag aga cac 423

Arg Cys Gln Thr Gly Glu Phe Leu Asp Thr Trp Asn Ala Glu Arg His

65

70

75

tgt cac cag cac aaa tac tgc gac ccc aac cta ggg ctc cat gtc gag 471

Cys His Gln His Lys Tyr Cys Asp Pro Asn Leu Gly Leu His Val Glu

80

85

90

aag gag ggc acg tca gaa aca gac acc act tgc aca tgc gat gaa ggt 519

Lys Glu Gly Thr Ser Glu Thr Asp Thr Thr Cys Thr Cys Asp Glu Gly

95

100

105

ctg cat tgt acc aac gct gcc tgt gag agc tgc acc atg cac agc ctg 567

Leu His Cys Thr Asn Ala Ala Cys Glu Ser Cys Thr Met His Ser Leu

110

115

120

tgc ccc cct ggc ctg gga gtc aaa cag atc gct aca ggg att tct gat 615

Cys Pro Pro Gly Leu Gly Val Lys Gln Ile Ala Thr Gly Ile Ser Asp

125

130

135

140

acc atc tgc gat ccc tgc ccc atc ggc ttc ttc tcc aat gtg tct tct 663

Thr Ile Cys Asp Pro Cys Pro Ile Gly Phe Phe Ser Asn Val Ser Ser

155

aaaaaaaaaa aaaaaaaaaa 1425

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 <212> PRT
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<400> 53

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 20 25 30

Val Asp Ser Gln Cys Cys Asn Met Cys Pro Pro Gly Glu Lys Leu Val
 35 40 45

Asn Asp Cys Leu His Thr Ile Asp Thr Glu Cys Thr Arg Cys Gln Thr
 50 55 60

Gly Glu Phe Leu Asp Thr Trp Asn Ala Glu Arg His Cys His Gln His
 65 70 75 80

Lys Tyr Cys Asp Pro Asn Leu Gly Leu His Val Glu Lys Glu Gly Thr
 85 90 95

Ser Glu Thr Asp Thr Thr Cys Thr Cys Asp Glu Gly Leu His Cys Thr
 100 105 110

Asn Ala Ala Cys Glu Ser Cys Thr Met His Ser Leu Cys Pro Pro Gly
 115 120 125

Leu Gly Val Lys Gln Ile Ala Thr Gly Ile Ser Asp Thr Ile Cys Asp
 130 135 140

Pro Cys Pro Ile Gly Phe Phe Ser Asn Val Ser Ser Ala Leu Glu Lys
 145 150 155 160

Cys His Pro Trp Thr Ser Cys Glu Thr Lys Gly Leu Val Lys Val Gln
 165 170 175

Ala Gly Thr Asn Lys Thr Asp Val Ile Cys Gly Pro Gln Pro Arg Leu
 180 185 190

Arg Ala Leu Val Val Val Pro Ile Ile Met Gly Ile Leu Leu Val Val
 195 200 205

Leu Leu Val Ser Ala Cys Ile Arg Lys Val Val Lys Lys Pro Glu Asn
 210 215 220

Lys Val Met Tyr Gln Asp Pro Val Glu Asp Leu Glu Glu Phe Pro Met
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Pro Pro His Ser Ile Ala Pro Val Gln Glu Thr Leu His Gly Cys Gln
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Arg Val

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<212> DNA
<213> Canis familiaris

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<212> DNA
<213> Canis familiaris

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tgcccaccag gagagaaact ggtgaatgac tgcctacata ccattgacac ggaatgcact 180
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tgtcaccott ggacaagctg tgaaacaaaa ggcctgggtga aggttcaggc gggaactaac 540
aagactgatg ttatctgtgg tcccagcct cggttaagag ccctagtggg ggtccccatc 600
attatgggga tcctgcttgt tgtcctgttg gtgtctgcct gcatccgaaa ggtggtcaag 660

215

aagccagaga ataaggttat gtatcaggac cctgtggagg acttggagga atttcctatg 720
 ccccgact ccattgctcc ggtgcaagag accttacatg ggtgccagcc cgtcaccag 780
 gaggacggca aagagagccg catctccgtg caggagagag tg 822

<210> 56
 <211> 822
 <212> DNA
 <213> Canis familiaris

<400> 56
 cactctctcc tgcacggaga tgcggctctc ttgcccgtcc tccctgggtga cgggctggca 60
 cccatgtaag gtctcttgca ccggagcaat ggagtgcggg ggcataggaa attcctccaa 120
 gtctccaca gggctctgat acataacctt attctctggc ttcttgacca cctttcggat 180
 gcaggcagac accaacagga caacaagcag gatccccata atgatgggga ccaccactag 240
 ggctcttaac cgaggctggg gaccacagat aacatcagtc ttgttagttc ccgcctgaac 300
 cttcaccagg cctttggttt cacagcttgt ccaagggtga cacttttcca aagcagaaga 360
 cacattggag aagaagccga tggggcaggg atcgcagatg gtatcagaaa tccctgtagc 420
 gatctgtttg actcccaggc caggggggca caggctgtgc atgggtgcagc tctcacaggc 480
 agcgttggtg caatgcagac ctcatcgca tgtgcaagtg gtgtctgttt ctgacgtgcc 540
 ctctttctcg acatggagcc ctaggttggg gtcgcagtat ttgtgctggt gacagtgtct 600
 ctctgcgttc caagtgtcta ggaattcgcc tgtttggcaa cgagtgcatt ccgtgtcaat 660
 ggtatgtagg cagtcattca ccagtttctc tccctgggtggg cacatattac agcactgact 720
 gtctactagg tattgctttt ctctgcatgc agtgcgtggt tctgggtaga cgggtgtcaa 780
 caaggagccc cagaagagac agcgcagagg caggagaacc at 822

<210> 57
 <211> 765
 <212> DNA
 <213> Canis familiaris

<220>

<221> CDS

<222> (1)..(765)

<400> 57

cca gaa cca cgc act gca tgc aga gaa aag caa tac cta gta gac agt 48

Pro Glu Pro Arg Thr Ala Cys Arg Glu Lys Gln Tyr Leu Val Asp Ser

1

5

10

15

cag tgc tgt aat atg tgc cca cca gga gag aaa ctg gtg aat gac tgc 96

Gln Cys Cys Asn Met Cys Pro Pro Gly Glu Lys Leu Val Asn Asp Cys

20

25

30

cta cat acc att gac acg gaa tgc act cgt tgc caa aca ggc gaa ttc 144

Leu His Thr Ile Asp Thr Glu Cys Thr Arg Cys Gln Thr Gly Glu Phe

35

40

45

cta gac act tgg aac gca gag aga cac tgt cac cag cac aaa tac tgc 192

Leu Asp Thr Trp Asn Ala Glu Arg His Cys His Gln His Lys Tyr Cys

50

55

60

gac ccc aac cta ggg ctc cat gtc gag aag gag ggc acg tca gaa aca 240

Asp Pro Asn Leu Gly Leu His Val Glu Lys Glu Gly Thr Ser Glu Thr

65

70

75

80

gac acc act tgc aca tgc gat gaa ggt ctg cat tgt acc aac gct gcc 288

Asp Thr Thr Cys Thr Cys Asp Glu Gly Leu His Cys Thr Asn Ala Ala

85

90

95

tgt gag agc tgc acc atg cac agc ctg tgc ccc cct ggc ctg gga gtc 336

Cys Glu Ser Cys Thr Met His Ser Leu Cys Pro Pro Gly Leu Gly Val

100

105

110

aaa cag atc gct aca ggg att tct gat acc atc tgc gat ccc tgc ccc 384

Lys Gln Ile Ala Thr Gly Ile Ser Asp Thr Ile Cys Asp Pro Cys Pro

115

120

125

atc ggc ttc ttc tcc aat gtg tct tct gct ttg gaa aag tgt cac cct 432

Ile Gly Phe Phe Ser Asn Val Ser Ser Ala Leu Glu Lys Cys His Pro

130

135

140

tgg aca agc tgt gaa acc aaa ggc ctg gtg aag gtt cag gcg gga act 480

Trp Thr Ser Cys Glu Thr Lys Gly Leu Val Lys Val Gln Ala Gly Thr

145

150

155

160

aac aag act gat gtt atc tgt ggt ccc cag cct cgg tta aga gcc cta 528

Asn Lys Thr Asp Val Ile Cys Gly Pro Gln Pro Arg Leu Arg Ala Leu

165

170

175

gatctgtttg actcccaggc caggggggca caggctgtgc atgggtgcagc tctcacaggc 480
agcgttggtg caatgcagac cttcatcgca tgtgcaagtg gtgtctgttt ctgacgtgcc 540
ctccttctcg acatggagcc ctaggttggg gtcgcagtat ttgtgctggt gacagtgtct 600
ctctgcgttc caagtgtcta ggaattcgcc tgtttggcaa cgagtgcatt ccgtgtcaat 660
ggtatgtagg cagtcattca ccagtttctc tcttggtggg cacatattac agcactgact 720
gtctactagg tattgctttt ctctgcatgc agtgcgtggt tctgg 765

<210> 60
<211> 336
<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (1)..(336)

<400> 60
aat gtg tca tct gct tcg gaa aag tgt cac cct tgg acg agg tgt gag 48
Asn Val Ser Ser Ala Ser Glu Lys Cys His Pro Trp Thr Arg Cys Glu
1 5 10 15
acc aaa ggc ctg gtg gag ctt cag gcg ggg acc aac aag acg gat gcc 96
Thr Lys Gly Leu Val Glu Leu Gln Ala Gly Thr Asn Lys Thr Asp Ala
20 25 30
gtc tgc ggt ttc cag gat cgg ata aga gcc ctg gtg gtg atc ccc atc 144
Val Cys Gly Phe Gln Asp Arg Ile Arg Ala Leu Val Val Ile Pro Ile
35 40 45
acg atg gtg gtc ctg ctt gct gtc ttg ttg gtg tct gcg tat atc aga 192
Thr Met Val Val Leu Leu Ala Val Leu Leu Val Ser Ala Tyr Ile Arg
50 55 60
aag gtg acc aag aag cca gag aat aag gtc ctc cag cct aag gct gtg 240
Lys Val Thr Lys Lys Pro Glu Asn Lys Val Leu Gln Pro Lys Ala Val
65 70 75 80
tcg cag gac cct gtg gag gac ttg gag gtc ctt cct gtc ccc ctc cac 288
Ser Gln Asp Pro Val Glu Asp Leu Glu Val Leu Pro Val Pro Leu His
85 90 95

ccaaggtga cacttttccg aagcagatga cacatt

336

<210> 63

<211> 390

<212> DNA

<213> Canis familiaris

<400> 63

ataagtgagg ctagtagtaa cccagcgtcc gttctgcggt gggcgccaaa aggtactac 60

accataagca gcaacctggt gagcctcgag aatgggaaac agttggccgt gaaaagacaa 120

ggactctatt acgtctatgc ccaagtcacc ttctgctcca atcgggcagc ttcgagtcaa 180

gctccgttcg tcgccagcct atgcctccat tccccgagtg gaacggagag agtcttactc 240

cgcgcgcga gctccgcgg ctcgtccaaa cttgcggcc aacagtccat ccaattggga 300

ggagtatttg aattgcatcc aggtgcttcg gtgttcgtca acgtgactga tccaagccaa 360

gtgagccacg ggaccggctt cacgtctttt 390

<210> 64

<211> 1878

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (284)..(1063)

<400> 64

aatgtatgga agaagaaact tgtttcttct ttactaacia aagggaaagc ctggaagtga 60

atgatatggg tataattaaa aaaaaaaaaa aaaaaaaaaa aaaaccttta cgtaactttt 120

tttgctggga gagaagacta cgaagcacat ttccaggaa gtgtgggctg caacgattgt 180

gcgctcttaa ctaatcctga gtaagggtggc cactttgaca gtgttttcat gctgcctctg 240

ccaccttctc ggtctgaaga tatcatttca actctaacac agc atg atc gaa aca 295

Met Ile Glu Thr

1

tat agc caa act gct ccc cga tct gtg gcc act gga cca ccc gtc agt 343

222

<400> 65

Met Ile Glu Thr Tyr Ser Gln Thr Ala Pro Arg Ser Val Ala Thr Gly
1 5 10 15

Pro Pro Val Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu
20 25 30

Ile Thr Gln Met Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg
35 40 45

Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu Tyr Glu Asp Phe Val
50 55 60

Phe Met Lys Thr Leu Gln Lys Cys Asn Lys Gly Glu Gly Ser Leu Ser
65 70 75 80

Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Ala Phe Leu Lys
85 90 95

Glu Ile Met Leu Asn Asn Glu Met Lys Lys Glu Glu Asn Ile Ala Met
100 105 110

Gln Lys Gly Asp Gln Asp Pro Arg Ile Ala Ala His Val Ile Ser Glu
115 120 125

Ala Ser Ser Asn Pro Ala Ser Val Leu Arg Trp Ala Pro Lys Gly Tyr
130 135 140

Tyr Thr Ile Ser Ser Asn Leu Val Ser Leu Glu Asn Gly Lys Gln Leu
145 150 155 160

Ala Val Lys Arg Gln Gly Leu Tyr Tyr Val Tyr Ala Gln Val Thr Phe
165 170 175

Cys Ser Asn Arg Ala Ala Ser Ser Gln Ala Pro Phe Val Ala Ser Leu
180 185 190

Cys Leu His Ser Pro Ser Gly Thr Glu Arg Val Leu Leu Arg Ala Ala
195 200 205

Ser Ser Arg Gly Ser Ser Lys Pro Cys Gly Gln Gln Ser Ile His Leu
210 215 220

Gly Gly Val Phe Glu Leu His Pro Gly Ala Ser Val Phe Val Asn Val
225 230 235 240

Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly

225

Leu Leu Lys Leu
260

<210> 66
<211> 1878
<212> DNA
<213> *Canis familiaris*

<400> 66
tttttttttt tttttttttt ttttttaacg ttaagggcgc tttattattc aaaaaataaa 60
taacaagata atcacaagtt cactctggaa acaatggaga ctgcaggtag gtaggagaga 120
tttcctttta atacagtcatt ttcaggagga ggagtgggca gcctctgctc tctcctcccg 180
cctacactgg tggagaggca acaggggtga aataagataa ccgattagca acagcctgac 240
tgtgggggga ggggggcgga ggaggagag aatgagtgtc agggtggtgt gtgggggcag 300
ggttttccag ttctccgcgc catcagactt tctggagcct gtcccctcca tcggggcccc 360
ggggaccccg ggtcaaccgt aactgactgt gagctgaggc tccctgttgc ccttcagcat 420
cttcgcgggg aaatcgagta cattctccag tgaaagacac tgcattgcaa gaaacaaaac 480
gaaactggac taattatctg ccgtttactg aggattcaat ctgtgcataa tagtctcgtc 540
tttttcatgg gactctctgg atgtctgcat cagtggggcg gctgcttcca gaatatcaac 600
tcttaccgac cggggcctgt tggcgctgcc cccgccctgt cattcccttc ttgcagccct 660
ccacgcctgg ggggtgtataa taaatagttc tccacgagga ggatcctagg gttataaata 720
ggcagttcaa caggggttgt ggtcttaact gctcggccgt attacgaaga ccaccaacag 780
gagctgagct gcagcctgtg aggtgccagc actcagagtt tgagtaagcc aaaagacgtg 840
aagccggtcc cgtggctcac ttggcttggg tcagtcacgt tgacgaacac cgaagcacct 900
ggatgcaatt caaatactcc tccaagtgg atggactgtt ggccgcaagg tttggacgag 960
ccgcgggagc tcgcggcgcg gagtaagact ctctccgttc cactcgggga atggaggcat 1020
aggctggcga cgaacggagc ttgactcgaa gctgcccgat tggagcagaa ggtgacttgg 1080

gcatagacgt aatagagtcc ttgtcttttc acggccaact gtttcccatt ctcgaggctc 1140
 accaggttgc tgcttatggg gtagtaccct tttggcgccc accgcagaac ggacgctggg 1200
 ttactactag cctcacttat gacatgggct gcaattcgag gatcctgac acctttttgc 1260
 attgcaatgt tttcttcttt cttcatttcg ttgttttagca ttatctcctt gagaaaggct 1320
 tcaaattggc ttttaatttc ctcacagttc agtaaggaca aggacccctc ccctttgttg 1380
 catttctgta acgttttcat gaacacaaaa tcttcataaa gattcctttc atcttctatc 1440
 ttgtccaatc ttctgtgaag atatacagca aagagtgccg atccaatcat ctgggtgatg 1500
 agaaaaacag taagcaaata cataaaaatt ttcatactga cgggtgggtcc agtggccaca 1560
 gatcgggggag cagtttgggt atatgtttcg atcatgctgt gttagagttg aaatgatatc 1620
 ttcagaccga gaaggtggca gaggcagcat gaaaacactg tcaaagtggc caccttactc 1680
 aggattagtt aagagcgcac aatcgttgca gccacactt cctggaaaat gtgcttcgta 1740
 gtcttctctc ccagcaaaaa aagttacgta aaggtttttt tttttttttt tttttttttt 1800
 taattatacc catatcattc acttccaggc tttccctttt gttagtaaag aagaaacaag 1860
 tttcttcttc catacatt 1878

<210> 67
 <211> 780
 <212> DNA
 <213> Canis familiaris

<400> 67
 atgatcgaac catatagcca aactgctccc cgatctgtgg ccaactggacc acccgtcagt 60
 atgaaaattt ttatgtattt gcttactgtt tttctcatca ccagatgat tggatcggca 120
 ctctttgctg tatatcttca cagaagattg gacaagatag aagatgaaag gaatctttat 180
 gaagattttg tgttcatgaa aacgttacag aaatgcaaca aaggggaggg gtccttgtcc 240
 ttactgaact gtgaggaaat taaaagccaa tttgaagcct ttctcaagga gataatgcta 300
 aacaacgaaa tgaagaaaga agaaaacatt gcaatgcaaa aaggtgatca ggatcctcga 360
 attgcagccc atgtcataag tgaggctagt agtaaccag cgtccgttct gcgggtggcg 420

ccaaaagggt actacaccat aagcagcaac ctggtgagcc tcgagaatgg gaaacagttg 480
gccgtgaaaa gacaaggact ctattacgtc tatgcccaag tcaccttctg ctccaatcgg 540
gcagcttcga gtcaagctcc gttcgtcgcc agcctatgcc tccattcccc gagtggaacg 600
gagagagtct tactccgcgc cgcgagctcc cgcggctcgt ccaaaccctg cggccaacag 660
tccatccact tgggaggagt atttgaattg catccagggtg cttcgggtgtt cgtcaacgtg 720
actgatccaa gccaaagtga ccacgggacc ggcttcacgt cttttggctt actcaaactc 780

<210> 68

<211> 780

<212> DNA

<213> Canis familiaris

<400> 68

gagtttgagt aagccaaaag acgtgaagcc ggtcccgtgg ctcaattggc ttggatcagt 60
cacgttgacg aacaccgaag cacctggatg caattcaaat actcctccca agtggatgga 120
ctgttggccg caaggtttgg acgagccgcg ggagctcgcg gcgcggagta agactctctc 180
cgttccactc ggggaatgga ggcataaggct ggcgacgaac ggagcttgac tcgaagctgc 240
ccgattggag cagaaggtga cttgggcata gacgtaatag agtccttgtc ttttcacggc 300
caactgtttc ccattctcga ggctcaccag gttgctgctt atgggtgtagt acccttttgg 360
cgcccaccgc agaacggacg ctgggttact actagcctca cttatgacat gggctgcaat 420
tcgaggatcc tgatcacctt tttgcattgc aatgttttct tctttcttca tttcgttggt 480
tagcattatc tccttgagaa aggcttcaaa ttggctttta atttcctcac agttcagtaa 540
ggacaaggac ccctcccctt tgttgcatth ctgtaacgtt ttcataaaca caaaatcttc 600
ataaagattc ctttcatctt ctatcttgtc caatcttctg tgaagatata cagcaaagag 660
tgccgatcca atcatctggg tgatgagaaa aacagtaagc aaatacataa aaattttcat 720
actgacgggt ggtccagtgg ccacagatcg gggagcagtt tggctatatg tttcgatcat 780

<210> 69

<211> 633
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(633)

<400> 69

ttg gac aag ata gaa gat gaa agg aat ctt tat gaa gat ttt gtg ttc 48
Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu Tyr Glu Asp Phe Val Phe
1 5 10 15

atg aaa acg tta cag aaa tgc aac aaa ggg gag ggg tcc ttg tcc tta 96
Met Lys Thr Leu Gln Lys Cys Asn Lys Gly Glu Gly Ser Leu Ser Leu
20 25 30

ctg aac tgt gag gaa att aaa agc caa ttt gaa gcc ttt ctc aag gag 144
Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Ala Phe Leu Lys Glu
35 40 45

ata atg cta aac aac gaa atg aag aaa gaa gaa aac att gca atg caa 192
Ile Met Leu Asn Asn Glu Met Lys Lys Glu Glu Asn Ile Ala Met Gln
50 55 60

aaa ggt gat cag gat cct cga att gca gcc cat gtc ata agt gag gct 240
Lys Gly Asp Gln Asp Pro Arg Ile Ala Ala His Val Ile Ser Glu Ala
65 70 75 80

agt agt aac cca gcg tcc gtt ctg cgg tgg gcg cca aaa ggg tac tac 288
Ser Ser Asn Pro Ala Ser Val Leu Arg Trp Ala Pro Lys Gly Tyr Tyr
85 90 95

acc ata agc agc aac ctg gtg agc ctc gag aat ggg aaa cag ttg gcc 336
Thr Ile Ser Ser Asn Leu Val Ser Leu Glu Asn Gly Lys Gln Leu Ala
100 105 110

gtg aaa aga caa gga ctc tat tac gtc tat gcc caa gtc acc ttc tgc 384
Val Lys Arg Gln Gly Leu Tyr Tyr Val Tyr Ala Gln Val Thr Phe Cys
115 120 125

tcc aat cgg gca gct tcg agt caa gct ccg ttc gtc gcc agc cta tgc 432
Ser Asn Arg Ala Ala Ser Ser Gln Ala Pro Phe Val Ala Ser Leu Cys
130 135 140

ctc cat tcc ccg agt gga acg gag aga gtc tta ctc cgc gcc gcg agc 480
Leu His Ser Pro Ser Gly Thr Glu Arg Val Leu Leu Arg Ala Ala Ser
145 150 155 160

229

tcc cgc ggc tcg tcc aaa cct tgc ggc caa cag tcc atc cac ttg gga 528
 Ser Arg Gly Ser Ser Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly
 165 170 175

gga gta ttt gaa ttg cat cca ggt gct tcg gtg ttc gtc aac gtg act 576
 Gly Val Phe Glu Leu His Pro Gly Ala Ser Val Phe Val Asn Val Thr
 180 185 190

gat cca agc caa gtg agc cac ggg acc ggc ttc acg tct ttt ggc tta 624
 Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu
 195 200 205

ctc aaa ctc 633
 Leu Lys Leu
 210

<210> 70
 <211> 211
 <212> PRT
 <213> Canis familiaris

<400> 70
 Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu Tyr Glu Asp Phe Val Phe
 1 5 10 15

Met Lys Thr Leu Gln Lys Cys Asn Lys Gly Glu Gly Ser Leu Ser Leu
 20 25 30

Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Ala Phe Leu Lys Glu
 35 40 45

Ile Met Leu Asn Asn Glu Met Lys Lys Glu Glu Asn Ile Ala Met Gln
 50 55 60

Lys Gly Asp Gln Asp Pro Arg Ile Ala Ala His Val Ile Ser Glu Ala
 65 70 75 80

Ser Ser Asn Pro Ala Ser Val Leu Arg Trp Ala Pro Lys Gly Tyr Tyr
 85 90 95

Thr Ile Ser Ser Asn Leu Val Ser Leu Glu Asn Gly Lys Gln Leu Ala
 100 105 110

Val Lys Arg Gln Gly Leu Tyr Tyr Val Tyr Ala Gln Val Thr Phe Cys
 115 120 125

230

Ser Asn Arg Ala Ala Ser Ser Gln Ala Pro Phe Val Ala Ser Leu Cys
 130 135 140

Leu His Ser Pro Ser Gly Thr Glu Arg Val Leu Leu Arg Ala Ala Ser
 145 150 155 160

Ser Arg Gly Ser Ser Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly
 165 170 175

Gly Val Phe Glu Leu His Pro Gly Ala Ser Val Phe Val Asn Val Thr
 180 185 190

Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu
 195 200 205

Leu Lys Leu
 210

<210> 71
 <211> 633
 <212> DNA
 <213> Canis familiaris

<400> 71
 gagtttgagt aagccaaaag acgtgaagcc ggtcccgtgg ctcaacttggc ttggatcagt 60
 cacgttgacg aacaccgaag cacctggatg caattcaaact actcctccca agtggatgga 120
 ctgttggccg caaggtttgg acgagccgcg ggagctcgcg gcgcggagta agactctctc 180
 cgttccactc ggggaatgga ggcataaggct ggcgacgaac ggagcttgac tcgaagctgc 240
 ccgattggag cagaaggtga cttgggcata gacgtaatag agtccttgtc ttttcacggc 300
 caactgtttc ccattctcga ggctcaccag gttgctgctt atgggtgtagt acccttttgg 360
 cgcccaccgc agaacggacg ctgggttact actagcctca cttatgacat gggctgcaat 420
 tcgaggatcc tgatcacctt tttgcattgc aatgttttct tctttcttca tttcgttggt 480
 tagcattatc tccttgagaa aggcttcaaa ttggctttta atttcctcac agttcagtaa 540
 ggacaaggac cctcccccctt tgttgcatth ctgtaacgtt ttcatagaaca caaatcttc 600
 ataaagattc ctttcatctt ctatcttgtc caa 633

[illegible][illegible][illegible]

607031

140

145

150

acc ctc gag aac ggg aag cag ctg gcc gtt aaa aga caa gga ctc tat 532
 Thr Leu Glu Asn Gly Lys Gln Leu Ala Val Lys Arg Gln Gly Leu Tyr
 155 160 165

tat atc tac gcc caa gtc acc ttc tgt tcc aat cgg gaa gct tcg agt 580
 Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser
 170 175 180

caa gct ccg ttc ata gcc agc ctc tgc ctg cat tcc ccg agt gga tcc 628
 Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu His Ser Pro Ser Gly Ser
 185 190 195 200

gag aga gtc tta ctc aga gct gca aat gcc cgc agt tcc tcc aaa ccc 676
 Glu Arg Val Leu Leu Arg Ala Ala Asn Ala Arg Ser Ser Ser Lys Pro
 205 210 215

tgt ggg cag caa tcc att cac ttg gga gga gtc ttc gaa ctg cat cca 724
 Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu His Pro
 220 225 230

ggg gct tcg gtg ttc gtg aac gtg act gat ccg agc caa gtg agc cac 772
 Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His
 235 240 245

ggg acg ggc ttc acg tct ttt ggc ttg ctc aaa ctc tgaacactgg 818
 Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu
 250 255 260

cacctcgag gccgcgaggc ctgcaggccg cggctgagct cacgctggga gtcttcacaa 878

tacagca 885

<210> 73
 <211> 260
 <212> PRT
 <213> Felis catus

<400> 73
 Met Ile Glu Thr Tyr Ser Gln Thr Ala Pro Arg Ser Val Ala Pro Gly
 1 5 10 15

Pro Pro Val Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu
 20 25 30

Ile Thr Gln Met Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg

233

35

40

45

Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu Tyr Glu Asp Phe Val
50 55 60

Phe Met Lys Thr Leu Gln Lys Cys Asn Lys Gly Glu Gly Ala Leu Ser
65 70 75 80

Leu Leu Asn Cys Glu Glu Ile Lys Ser Arg Phe Glu Ala Phe Leu Lys
85 90 95

Glu Ile Met Leu Asn Lys Glu Thr Lys Lys Glu Lys Asn Val Ala Met
100 105 110

Gln Lys Gly Asp Gln Asp Pro Arg Val Ala Ala His Val Ile Ser Glu
115 120 125

Ala Ser Ser Ser Thr Ala Ser Val Leu Gln Trp Ala Pro Lys Gly Tyr
130 135 140

Tyr Thr Ile Ser Ser Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu
145 150 155 160

Ala Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe
165 170 175

Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu
180 185 190

Cys Leu His Ser Pro Ser Gly Ser Glu Arg Val Leu Leu Arg Ala Ala
195 200 205

Asn Ala Arg Ser Ser Ser Lys Pro Cys Gly Gln Gln Ser Ile His Leu
210 215 220

Gly Gly Val Phe Glu Leu His Pro Gly Ala Ser Val Phe Val Asn Val
225 230 235 240

Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly
245 250 255

Leu Leu Lys Leu
260

<210> 74
<211> 885
<212> DNA

<213> Felis catus

<400> 74

tgctgtatta tgaagactcc cagcgtgagc tcagccgcgg cctgcaggcc tcgcggcctg 60
cgaggtgcc a gtgttcagag tttgagcaag ccaaaagacg tgaagcccgt cccgtggctc 120
acttggtctg gatcagtcac gttcacgaac accgaagcac ctggatgcag ttcgaagact 180
cctcccaagt gaatggattg ctgcccacag ggtttgagg aactgcgggc atttgagct 240
ctgagtaaga ctctctcgga tccactcggg gaatgcaggc agaggctggc tatgaacgga 300
gcttgactcg aagcttcccg attggaacag aagggtgactt gggcgtagat ataataagagt 360
ccttgtcttt taacggccag ctgcttcccg ttctcgaggg tcaccaagtt gctgcttatg 420
gtgtagtagc ctttgggggc cactggaga acagacgctg tgctactgct ggcctcactt 480
atgacatgtg ctgcaactcg aggatcctgg tcgccttttt gcattgcaac atttttttct 540
ttcttcgttt ctttgttttag cattatctcc ttgagaaagg cttcaaaccg gcttttaatt 600
tcctcacagt tcagtaagga taaggccccc tctcctttgt tgcatttctg taatgttttc 660
atgaacacaa aatcttcata aagattcctt tcactttcta tcttgccag tcttctgtga 720
agatacacag caaagagtgc tgacccaatc atctgggtga tgagaaacac agtaagtaaa 780
tacataaaaa ttttcatact gacgggtggt ccaggggcca cggagcgggg agcagtttgg 840
ctatatgttt cgatcatgct gtgttaaagt tgaaatggta tcttc 885

<210> 75

<211> 780

<212> DNA

<213> Felis catus

<400> 75

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atgaaaattt ttatgtattt acttactgtg tttctcatca cccagatgat tgggtcagca 120
ctctttgctg tgtatcttca cagaagactg gacaagatag aagatgaaag gaatctttat 180
gaagattttg tgttcatgaa aacattacag aaatgcaaca aaggagaggg ggccttatcc 240

235

ttactgaact gtgaggaaat taaaagccgg tttgaagcct ttctcaagga gataatgcta 300
 aacaaagaaa cgaagaaaga aaaaaatggt gcaatgcaaa aaggcgacca ggatcctcga 360
 gttgcagcac atgtcataag tgaggccagc agtagcacag cgtctgttct ccagtgggcc 420
 cccaaaggct actacaccat aagcagcaac ttggtgaccc tcgagaacgg gaagcagctg 480
 gccgttaaaa gacaaggact ctattatatc tacgcccaag tcaccttctg ttccaatcgg 540
 gaagcttcga gtcaagctcc gttcatagcc agcctctgcc tgcattcccc gagtggatcc 600
 gagagagtct tactcagagc tgcaaatgcc cgcagttcct ccaaaccctg tgggcagcaa 660
 tccattcact tgggaggagt cttcgaactg catccaggtg cttcggtgtt cgtgaacgtg 720
 actgatccga gccaaagtga ccacggggacg ggcttcacgt cttttggctt gctcaaaactc 780

<210> 76
 <211> 780
 <212> DNA
 <213> Felis catus

<400> 76
 gagtttgagc aagccaaaag acgtgaagcc cgtcccgtgg ctcaattggc tcggatcagt 60
 cacgttcacg aacaccgaag cacctggatg cagttcgaag actcctccca agtgaatgga 120
 ttgctgcca cagggtttgg aggaactgcg ggcatttgca gctctgagta agactctctc 180
 ggatccactc ggggaatgca ggcagaggct ggctatgaac ggagcttgac tcgaagcttc 240
 ccgattggaa cagaagggtga cttgggcgta gatataatag agtccttgtc ttttaacggc 300
 cagctgcttc ccgttctcga gggtcaccaa gttgctgctt atggtgtagt agcctttggg 360
 ggcccactgg agaacagacg ctgtgctact gctggcctca cttatgacat gtgctgcaac 420
 tcgaggatcc tggtcgcctt ttgcatgac aacatttttt tctttcttcg tttctttgtt 480
 tagcattatc tccttgagaa aggcttcaaa ccggctttta atttctcac agttcagtaa 540
 ggataaggcc ccctctcctt tgttgcatth ctgtaatggt ttcattgaaca caaaatcttc 600
 ataaagattc ctttcatctt ctatcttgtc cagtcttctg tgaagataca cagcaaagag 660
 tgctgacca atcatctggg tgatgagaaa cacagtaagt aaatacataa aaattttcat 720

actgacgggt ggtccagggg ccacggagcg gggagcagtt tggctatatg tttcgatcat 780

<210> 77
<211> 633
<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (1)..(633)

<400> 77

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1 5 10 15

atg aaa aca tta cag aaa tgc aac aaa gga gag ggg gcc tta tcc tta 96
Met Lys Thr Leu Gln Lys Cys Asn Lys Gly Glu Gly Ala Leu Ser Leu
20 25 30

ctg aac tgt gag gaa att aaa agc cgg ttt gaa gcc ttt ctc aag gag 144
Leu Asn Cys Glu Glu Ile Lys Ser Arg Phe Glu Ala Phe Leu Lys Glu
35 40 45

ata atg cta aac aaa gaa acg aag aaa gaa aaa aat gtt gca atg caa 192
Ile Met Leu Asn Lys Glu Thr Lys Lys Glu Lys Asn Val Ala Met Gln
50 55 60

aaa ggc gac cag gat cct cga gtt gca gca cat gtc ata agt gag gcc 240
Lys Gly Asp Gln Asp Pro Arg Val Ala Ala His Val Ile Ser Glu Ala
65 70 75 80

agc agt agc aca gcg tct gtt ctc cag tgg gcc ccc aaa ggc tac tac 288
Ser Ser Ser Thr Ala Ser Val Leu Gln Trp Ala Pro Lys Gly Tyr Tyr
85 90 95

acc ata agc agc aac ttg gtg acc ctc gag aac ggg aag cag ctg gcc 336
Thr Ile Ser Ser Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Ala
100 105 110

gtt aaa aga caa gga ctc tat tat atc tac gcc caa gtc acc ttc tgt 384
Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys
115 120 125

tcc aat cgg gaa gct tcg agt caa gct ccg ttc ata gcc agc ctc tgc 432
Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys

130

135

140

ctg cat tcc ccg agt gga tcc gag aga gtc tta ctc aga gct gca aat 480
 Leu His Ser Pro Ser Gly Ser Glu Arg Val Leu Leu Arg Ala Ala Asn
 145 150 155 160

gcc cgc agt tcc tcc aaa ccc tgt ggg cag caa tcc att cac ttg gga 528
 Ala Arg Ser Ser Ser Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly
 165 170 175

gga gtc ttc gaa ctg cat cca ggt gct tcg gtg ttc gtg aac gtg act 576
 Gly Val Phe Glu Leu His Pro Gly Ala Ser Val Phe Val Asn Val Thr
 180 185 190

gat ccg agc caa gtg agc cac ggg acg ggc ttc acg tct ttt ggc ttg 624
 Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu
 195 200 205

ctc aaa ctc 633
 Leu Lys Leu
 210

<210> 78
 <211> 211
 <212> PRT
 <213> Felis catus

<400> 78
 Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu Tyr Glu Asp Phe Val Phe
 1 5 10 15

Met Lys Thr Leu Gln Lys Cys Asn Lys Gly Glu Gly Ala Leu Ser Leu
 20 25 30

Leu Asn Cys Glu Glu Ile Lys Ser Arg Phe Glu Ala Phe Leu Lys Glu
 35 40 45

Ile Met Leu Asn Lys Glu Thr Lys Lys Glu Lys Asn Val Ala Met Gln
 50 55 60

Lys Gly Asp Gln Asp Pro Arg Val Ala Ala His Val Ile Ser Glu Ala
 65 70 75 80

Ser Ser Ser Thr Ala Ser Val Leu Gln Trp Ala Pro Lys Gly Tyr Tyr
 85 90 95

Thr Ile Ser Ser Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Ala

ggataaggcc ccctctcctt tgttgcattt ctgtaatggt ttcatagaaca caaaatcttc 600

ataaagattc ctttcatctt ctatcttgtc cag 633

<210> 80

<211> 610

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (29)..(430)

<400> 80

caaggcaaac actgaacatt tcagagct atg aga atg ctt ctg aat ttg agt 52
Met Arg Met Leu Leu Asn Leu Ser
1 5

ttg cta gct ctt ggg gct gcc tat gtt tct gcc ttt gct gta gaa aat 100
Leu Leu Ala Leu Gly Ala Ala Tyr Val Ser Ala Phe Ala Val Glu Asn
10 15 20

ccc atg aat aga ctg gtg gca gag acc ttg aca ctg ctc tcc act cat 148
Pro Met Asn Arg Leu Val Ala Glu Thr Leu Thr Leu Leu Ser Thr His
25 30 35 40

cga act tgg ctg ata ggc gat ggg aac ctg atg att cct act cct gaa 196
Arg Thr Trp Leu Ile Gly Asp Gly Asn Leu Met Ile Pro Thr Pro Glu
45 50 55

aat aaa aat cac caa ctg tgc att aaa gaa gtt ttt cag ggt ata gac 244
Asn Lys Asn His Gln Leu Cys Ile Lys Glu Val Phe Gln Gly Ile Asp
60 65 70

aca ttg aag aac caa act gcc cac ggg gag gct gtg gat aaa cta ttc 292
Thr Leu Lys Asn Gln Thr Ala His Gly Glu Ala Val Asp Lys Leu Phe
75 80 85

caa aac ttg tct tta ata aaa gaa cac ata gag cgc caa aaa aaa agg 340
Gln Asn Leu Ser Leu Ile Lys Glu His Ile Glu Arg Gln Lys Lys Arg
90 95 100

tgt gca gga gaa aga tgg aga gtg aca aag ttc cta gac tac ctg caa 388
Cys Ala Gly Glu Arg Trp Arg Val Thr Lys Phe Leu Asp Tyr Leu Gln
105 110 115 120

gta ttt ctt ggt gta ata aac acc gag tgg aca ccg gaa agt 430

[illegible]

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<210> 81
<211> 134
<212> PRT
<213> Canis familiaris
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Val Ser Ala Phe Ala Val Glu Asn Pro Met Asn Arg Leu Val Ala Glu
20 25 30

Asn Leu Met Ile Pro Thr Pro Glu Asn Lys Asn His Gln Leu Cys Ile
50 55 60

Lys Glu Val Phe Gln Gly Ile Asp Thr Leu Lys Asn Gln Thr Ala His
65 70 75 80

Gly Glu Ala Val Asp Lys Leu Phe Gln Asn Leu Ser Leu Ile Lys Glu
85 90 95

His Ile Glu Arg Gln Lys Lys Arg Cys Ala Gly Glu Arg Trp Arg Val
100 105 110

Thr Lys Phe Leu Asp Tyr Leu Gln Val Phe Leu Gly Val Ile Asn Thr
115 120 125

Glu Trp Thr Pro Glu Ser
130

71

241

<400> 82

ctcaaata tttcatctgt gtgaagtgat aaagtagtag gatgcctgaa atatttactt 60
 tgtctctgaa gcttagttat actggccatt aagtcctac tgttggttgg ccctcattct 120
 catcgccaaa aaaccattct tctccaaaat cttccactac aataagccgg tttgttctca 180
 actttccggg gtccactcgg tgtttattac accaagaaat acttgcaggt agtctaggaa 240
 ctttgtcact ctccatcttt ctctgcaca cttttttttt tggcgctcta tgtgttcttt 300
 tattaagac aagttttgga atagtttata cacagcctcc ccgtgggcag tttggttctt 360
 caatgtgtct ataccctgaa aaacttcttt aatgcacagt tgggtgatttt tattttcagg 420
 agtaggaatc atcaggttcc catcgccat cagccaagtt cgatgagtgg agagcagtgt 480
 caaggtctct gccaccagtc tattcatggg attttctaca gcaaaggcag aaacataggc 540
 agccccaaga gctagcaaac tcaaattcag aagcattctc atagctctga aatgttcagt 600
 gtttgccttg 610

<210> 83

<211> 402

<212> DNA

<213> Canis familiaris

<400> 83

atgagaatgc ttctgaattt gagtttgcta gctcttgggg ctgcctatgt ttctgccttt 60
 gctgtagaaa atcccatgaa tagactggtg gcagagacct tgacactgct ctccactcat 120
 cgaacttggc tgataggcga tgggaacctg atgattccta ctctgaaaa taaaaatcac 180
 caactgtgca ttaaagaagt ttttcagggt atagacacat tgaagaacca aactgcccac 240
 ggggaggctg tggataaact attccaaaac ttgtctttta taaaagaaca catagagcgc 300
 caaaaaaaaaa ggtgtgcagg agaaagatgg agagtgcaca agttcctaga ctacctgcaa 360
 gtatttcttg gtgtaataaa caccgagtgg acaccggaaa gt 402

<210> 84

<211> 402

<212> DNA

<213> Canis familiaris

<400> 84

actttccggt gtccactcgg tgtttattac accaagaaat acttgcaggt agtctaggaa 60
ctttgtcact ctccatcttt ctctgcaca cctttttttt tggcgcctcta tgtgttcttt 120
tattaaagac aagttttgga atagtttata cacagcctcc ccgtgggcag tttggttctt 180
caatgtgtct ataccctgaa aaacttcttt aatgcacagt tggtgatttt tattttcagg 240
agtaggaatc atcaggttcc catgcctat cagccaagtt cgatgagtgg agagcagtgt 300
caaggtctct gccaccagtc tattcatggg attttctaca gcaaaggcag aaacataggc 360
agccccaaga gctagcaaac tcaaattcag aagcattctc at 402

<210> 85

<211> 345

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (1)..(345)

<400> 85

ttt gct gta gaa aat ccc atg aat aga ctg gtg gca gag acc ttg aca 48
Phe Ala Val Glu Asn Pro Met Asn Arg Leu Val Ala Glu Thr Leu Thr
1 5 10 15
ctg ctc tcc act cat cga act tgg ctg ata ggc gat ggg aac ctg atg 96
Leu Leu Ser Thr His Arg Thr Trp Leu Ile Gly Asp Gly Asn Leu Met
20 25 30
att cct act cct gaa aat aaa aat cac caa ctg tgc att aaa gaa gtt 144
Ile Pro Thr Pro Glu Asn Lys Asn His Gln Leu Cys Ile Lys Glu Val
35 40 45
ttt cag ggt ata gac aca ttg aag aac caa act gcc cac ggg gag gct 192
Phe Gln Gly Ile Asp Thr Leu Lys Asn Gln Thr Ala His Gly Glu Ala
50 55 60
gtg gat aaa cta ttc caa aac ttg tct tta ata aaa gaa cac ata gag 240
Val Asp Lys Leu Phe Gln Asn Leu Ser Leu Ile Lys Glu His Ile Glu
65 70 75 80

cgc caa aaa aaa agg tgt gca gga gaa aga tgg aga gtg aca aag ttc 288
 Arg Gln Lys Lys Arg Cys Ala Gly Glu Arg Trp Arg Val Thr Lys Phe
 85 90 95

cta gac tac ctg caa gta ttt ctt ggt gta ata aac acc gag tgg aca 336
 Leu Asp Tyr Leu Gln Val Phe Leu Gly Val Ile Asn Thr Glu Trp Thr
 100 105 110

ccg gaa agt 345
 Pro Glu Ser
 115

<210> 86
 <211> 115
 <212> PRT
 <213> Canis familiaris

<400> 86
 Phe Ala Val Glu Asn Pro Met Asn Arg Leu Val Ala Glu Thr Leu Thr
 1 5 10 15

Leu Leu Ser Thr His Arg Thr Trp Leu Ile Gly Asp Gly Asn Leu Met
 20 25 30

Ile Pro Thr Pro Glu Asn Lys Asn His Gln Leu Cys Ile Lys Glu Val
 35 40 45

Phe Gln Gly Ile Asp Thr Leu Lys Asn Gln Thr Ala His Gly Glu Ala
 50 55 60

Val Asp Lys Leu Phe Gln Asn Leu Ser Leu Ile Lys Glu His Ile Glu
 65 70 75 80

Arg Gln Lys Lys Arg Cys Ala Gly Glu Arg Trp Arg Val Thr Lys Phe
 85 90 95

Leu Asp Tyr Leu Gln Val Phe Leu Gly Val Ile Asn Thr Glu Trp Thr
 100 105 110

Pro Glu Ser
 115

<210> 87
 <211> 345
 <212> DNA

<213> Canis familiaris

<400> 87

actttccggt gtccactcgg tgtttattac accaagaaat acttgcaggt agtctaggaa 60
ctttgtcaact ctccatcttt ctccctgcaca cctttttttt tggcgctcta tgtgttcttt 120
tattaaagac aagttttgga atagtttata cacagcctcc ccgtgggcag tttggttctt 180
caatgtgtct ataccctgaa aaacttcttt aatgcacagt tgggtgatttt tattttcagg 240
agtaggaatc atcaggttcc catcgctat cagccaagtt cgatgagtgg agagcagtgt 300
caaggtctct gccaccagtc tattcatggg attttctaca gcaaa 345

<210> 88

<211> 166

<212> DNA

<213> Canis familiaris

<400> 88

ctcagcttag gccagcctac gacctgcctg ctcttccctc gtcctcctg cattggctct 60
gggctccatg gcgctctggt tgactgtggt cattgctctc acctgcctcg gtggccttgc 120
ctccccgagc cctgtgactc cctccccaac cctcaaggag ctcat 166

<210> 89

<211> 272

<212> DNA

<213> Canis familiaris

<400> 89

tggccttgcc tccccgagcc ctgtgactcc ctccccaacc ctcaaggagc tcattgagga 60
gctggtcaac atcaccaga atcaggcatc cctctgcaac ggcagcatgg tgtggagcgt 120
caacctgacc gccggcatgt actgcgcagc tctagaatct ctgatcaatg tctccgactg 180
cagcgccatc caaaggaccc agaggatgct gaaagcactg tgctctcaaa agcccgcggc 240
agggcagatt tccagtgaac gcagccgaga ca 272

<210> 90

<211> 278

245

<212> DNA

<213> Canis familiaris

<400> 90

atggcgctct ggttgactgt ggtcattgct ctcacctgcc tcggtggcct tgcctccccg 60
agccctgtga ctccctcccc aacctcaag gagctcattg aggagctggt caacatcacc 120
cagaatcagg catccctctg caacggcagc atggtgtgga gcgtaacct gaccgccggc 180
atgtactgcg cagctctaga atctctgac aatgtctccg actgcagcgc catccaaagg 240
accagagga tgctgaaagc actgtgctct caaaagcc 278

<210> 91

<211> 1302

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (52)..(444)

<400> 91

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Met Ala
1
ctc tgg ttg act gtg gtc att gct ctc acc tgc ctc ggt ggc ctt gcc 105
Leu Trp Leu Thr Val Val Ile Ala Leu Thr Cys Leu Gly Gly Leu Ala
5 10 15
tcc ccg agc cct gtg act ccc tcc cca acc ctc aag gag ctc att gag 153
Ser Pro Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu Ile Glu
20 25 30
gag ctg gtc aac atc acc cag aat cag gca tcc ctc tgc aac ggc agc 201
Glu Leu Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn Gly Ser
35 40 45 50
atg gtg tgg agc gtc aac ctg acc gcc ggc atg tac tgc gca gct cta 249
Met Val Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu
55 60 65
gaa tct ctg atc aat gtc tcc gac tgc agc gcc atc caa agg acc cag 297
Glu Ser Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg Thr Gln
70 75 80

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agg atg ctg aaa gca ctg tgc tct caa aag ccc gcg gca ggg cag att 345
Arg Met Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly Gln Ile
      85                90                95

tcc agt gaa cgc agc cga gac acc aaa att gaa gtg atc cag ttg gtg 393
Ser Ser Glu Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu Val
      100              105              110

aaa aac ctg ctc acc tat gta agg gga gtt tat cgc cat gga aat ttc 441
Lys Asn Leu Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn Phe
      115              120              125              130

aga tgaagcatga aaacttagca tccttatctg tagaccacaga cctgaccact 494
Arg

taagttccag attcattttt ctttccgacg tcacaaattt cttagggagg tggggggggg 554

ggagaacccat ttcttcagct gggacctcag cctgcaccgc ctgcctccat ggagctgagc 614

ccagccaccc ctgccttggt gcatggggcc cagccgggtg gccctcctcc gtctgcactt 674

catcaacgct gagggaaagc actgcatccc atgactgtcc cctcctcaga gcaaagtgca 734

gcattacagt ggaggcagat atgtgtggga gggggtcttg ctgtacctgg gagtggcaca 794

gacatgtttc ttcttagcct tatttattat tgtgtgttat ttaaacaagt gtctttgttt 854

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ctgggaataa gcactgtgtg taaaattctg ctacctcact gggatcctgg ggccgacaca 974

ggggacagga gaaaggggtca gagatgctgc ttttgtctgc cactcagcag ctggccctca 1034

gccaagcagt aatttattgt ttttccttgt atttaaagtt aagaaataaa atatgttatc 1094

aaagagttaa taatatatag aagagtagcc taaaaggctg catttggtgt gtgtggccag 1154

gccggggcgg gtggggggga ggggtgtgtc actgaatgtg ctctttcact gactttgtca 1214

aactggaagc cagaaataaa gatggtgaca agagaaaaaa aaaaaaaaaa aaaaaaaaaa 1274

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1302

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<210> 92
 <211> 131
 <212> PRT

<213> Canis familiaris

<400> 92

Met Ala Leu Trp Leu Thr Val Val Ile Ala Leu Thr Cys Leu Gly Gly
1 5 10 15

Leu Ala Ser Pro Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu
20 25 30

Ile Glu Glu Leu Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn
35 40 45

Gly Ser Met Val Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala
50 55 60

Ala Leu Glu Ser Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg
65 70 75 80

Thr Gln Arg Met Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly
85 90 95

Gln Ile Ser Ser Glu Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln
100 105 110

Leu Val Lys Asn Leu Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly
115 120 125

Asn Phe Arg
130

<210> 93

<211> 1302

<212> DNA

<213> Canis familiaris

<400> 93

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caacaccctc cccccaccc gccccggcct ggccacacac accaaatgca gccttttagg 180

ctactcttct atatattatt aactctttga taacatattt tatttcttaa ctttaaatac 240

aaggaaaaac aataaattac tgcttggttg agggccagct gctgagtggc agacaagagc 300

agcatctctg accctttctc ctgtcccctg tgtcggcccc aggatcccag tgaggtagca 360

gaattttaca cacagtgtt attcccaggg actctctaaa cccgagtcac tgggccccca 420
gctccaagcc actccctgtc cccagcacaa acaaagacac ttgtttaaat aacacacaat 480
aataaataag gctaagaaga aacatgtctg tgccactccc aggtacagca agacccccctc 540
ccacacatat ctgcctccac tgtaatgtct cactttgtct tgaggagggg acagtcattg 600
gatgcagtgc ttccctcag cgttgatgaa gtgcagacgg aggagggcca cccggctggg 660
cccatgcac caaggcaggg gtggctgggc tcagctccat ggaggcaggc ggtgcaggct 720
gaggtcccag ctgaggaaat ggttctcccc cccccccacc tccctaagaa atttgtgacg 780
tcggaaagaa aaatgaatct ggaacttaag tggtcaggct tgggtctaca gataaggatg 840
ctaagttttc atgtttcatc tgaaatttcc atggcgataa actcccctta cataggtgag 900
caggtttttc accaactgga tcacttcaat ttgtgtgtct cggctgcgtt cactggaaat 960
ctgccctgcc gggggctttt gagagcacag tgctttcagc atcctctggg tcctttggat 1020
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caggttgacg ctccacacca tgctgccgtt gcagagggat gcctgattct gggatgatgtt 1140
gaccagctcc tcaatgagct ccttgagggt tggggaggga gtcacagggc tcggggaggc 1200
aaggccaccg aggcagggtga gagcaatgac cacagtcaac cagagcgcca tggagcccag 1260
agccaatgca ggaggagcga gggaagagca ggcaggctcg ag 1302

<210> 94
<211> 393
<212> DNA
<213> Canis familiaris

<400> 94
atggcgctct ggttgactgt ggtcattgct ctacctgcc tcggtggcct tgcctccccg 60
agccctgtga ctccctcccc aacctcaag gagctcattg aggagctggg caacatcacc 120
cagaatcagg catccctctg caacggcagc atgggtgtgga gcgtcaacct gaccgccggc 180
atgtactgcg cagctctaga atctctgatc aatgtctccg actgcagcgc catccaaagg 240

accagagga tgctgaaagc actgtgctct caaaagcccg cggcagggca gatttccagt 300
gaacgcagcc gagacaccaa aattgaagtg atccagttgg tgaaaaacct gctcacctat 360
gtaaggggag tttatcgcca tggaaatttc aga 393

<210> 95
<211> 393
<212> DNA
<213> Canis familiaris

<400> 95
tctgaaattt ccatggcgat aaactccoct tacataggtg agcaggtttt tcaccaactg 60
gatcacttca attttggtgt ctcggtgcg ttcactggaa atctgccctg ccgcgggctt 120
ttgagagcac agtgctttca gcatcctctg ggtcctttgg atggcgctgc agtcggagac 180
attgatcaga gattctagag ctgcgcagta catgccggcg gtcaggttga cgctccacac 240
catgctgccg ttgcagaggg atgcctgatt ctgggtgatg ttgaccagct cctcaatgag 300
ctccttgagg gttggggagg gagtcacagg gctcggggag gcaaggccac cgaggcaggt 360
gagagcaatg accacagtca accagagcgc cat 393

<210> 96
<211> 333
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(333)

<400> 96
agc cct gtg act ccc tcc cca acc ctc aag gag ctc att gag gag ctg 48
Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu Ile Glu Glu Leu
1 5 10 15
gtc aac atc acc cag aat cag gca tcc ctc tgc aac ggc agc atg gtg 96
Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn Gly Ser Met Val
20 25 30
tgg agc gtc aac ctg acc gcc ggc atg tac tgc gca gct cta gaa tct 144
Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu Glu Ser

35

40

45

ctg atc aat gtc tcc gac tgc agc gcc atc caa agg acc cag agg atg 192
 Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg Thr Gln Arg Met
 50 55 60

ctg aaa gca ctg tgc tct caa aag ccc gcg gca ggg cag att tcc agt 240
 Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly Gln Ile Ser Ser
 65 70 75 80

gaa cgc agc cga gac acc aaa att gaa gtg atc cag ttg gtg aaa aac 288
 Glu Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu Val Lys Asn
 85 90 95

ctg ctc acc tat gta agg gga gtt tat cgc cat gga aat ttc aga 333
 Leu Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn Phe Arg
 100 105 110

<210> 97

<211> 111

<212> PRT

<213> Canis familiaris

<400> 97

Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu Ile Glu Glu Leu
 1 5 10 15

Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn Gly Ser Met Val
 20 25 30

Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu Glu Ser
 35 40 45

Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg Thr Gln Arg Met
 50 55 60

Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly Gln Ile Ser Ser
 65 70 75 80

Glu Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu Val Lys Asn
 85 90 95

Leu Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn Phe Arg
 100 105 110

<210> 98

25!

<211> 333
 <212> DNA
 <213> Canis familiaris

<400> 98
 tctgaaattt ccatggcgat aaactccctt tacataggtg agcagggttt tcaccaactg 60
 gatcacttca attttggtgt ctcggtgcg ttactggaa atctgccctg ccgcgggctt 120
 ttgagagcac agtgctttca gcactcctctg ggctccttgg atggcgctgc agtcggagac 180
 attgatcaga gattctagag ctgcgcagta catgccggcg gtcagggtga cgctccacac 240
 catgctgccg ttgcagaggg atgcctgatt ctgggtgatg ttgaccagct cctcaatgag 300
 ctcttgagg gttggggagg gagtacaggg gct 333

<210> 99
 <211> 1269
 <212> DNA
 <213> Canis familiaris

<220>
 <221> CDS
 <222> (57)..(446)

<400> 99
 ccagcctacg acctgcctgc tcttccctcg ctctcctgc attggtctg ggctcc atg 59
 Met
 1
 gcg ctc tgg ttg act gtg gtc att gct ctc acc tgc ctc ggt ggc ctt 107
 Ala Leu Trp Leu Thr Val Val Ile Ala Leu Thr Cys Leu Gly Gly Leu
 5 10 15
 gcc tcc ccg agc cct gtg act ccc tcc cca acc ctc aag gag ctc att 155
 Ala Ser Pro Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu Ile
 20 25 30
 gag gag ctg gtc aac atc acc cag aat cag gca tcc ctc tgc aac ggc 203
 Glu Glu Leu Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn Gly
 35 40 45
 agc atg gtg tgg agc gtc aac ctg acc gcc ggc atg tac tgc gca gct 251
 Ser Met Val Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
 50 55 60 65

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Phe Arg
130

<400> 101

84

254

gccccaggat cccagtgagg tagcagaatt ttacacacag tgcttattcc cagggactct 360
ctaaaccgga gtcactgggc ccccagctcc aagccactcc ctgtccccag cacaaacaaa 420
gacacttggt taaataacac acaataataa ataaggctaa gaagaaacat gtctgtgcca 480
ctcccaggta cagcaagacc ccctcccaca catatctgcc tccactgtaa tgctgcactt 540
tgctctgagg aggggacagt catgggatgc agtgctttcc ctcagcgttg atgaagtgca 600
gacggaggag ggccacccgg ctgggccccca tgcaccaagg caggggtggc tgggctcagc 660
tccatggagg caggcgggtgc aggctgaggt cccagctgag gaaatgggtc tcccccccc 720
ccacctccct aagaaatttg tgacgtcgga aagaaaaatg aatctggaac ttaagtggtc 780
aggctctgggt ctacagataa ggatgctaag ttttcatgct tcatctgaaa tttccatggc 840
gataaactcc ccttacatag gtgagcaggt ttttcaccaa ctggatcact tcaatttttg 900
tgtctcggct gcgttactg gaaatccctg ccgcgggctt ttgagagcac agtgctttca 960
gcacccctctg ggctcctttg atggcgctgc agtcggagac attgatcaga gattctagag 1020
ctgcgcagta catgccggcg gtcagggtga cgctccacac catgctgccg ttgcagaggg 1080
atgcctgatt ctgggtgatg ttgaccagct cctcaatgag ctccctgagg gttggggagg 1140
gagtcacagg gctcggggag gcaaggccac cgaggcaggt gagagcaatg accacagtca 1200
accagagcgc catggagccc agagccaatg caggaggagc gagggaagag caggcaggtc 1260
gtaggctgg 1269

<210> 102
<211> 390
<212> DNA
<213> Canis familiaris

<400> 102
atggcgctct ggttgactgt ggtcattgct ctacactgcc tcggtggcct tgcctccccg 60
agccctgtga ctccctcccc aaccctcaag gagctcattg aggagctggt caacatcacc 120
cagaatcagg catccctctg caacggcagc atgggtgtgga gcgtcaacct gaccgccggc 180

atgtactgcg cagctctaga atctctgac aatgtctccg actgcagcgc catccaaagg 240
 acccagagga tgctgaaagc actgtgctct caaaagccccg cggcagggat ttccagtga 300
 cgcagccgag acacccaaat tgaagtgatc cagttgggtga aaaacctgct cacctatgta 360
 aggggagttt atcgccatgg aaatttcaga 390

<210> 103
 <211> 390
 <212> DNA
 <213> Canis familiaris

<400> 103
 tctgaaattt ccatggcgat aaactcccct tacataggtg agcaggtttt tcaccaactg 60
 gatcacttca attttgggtgt ctcggctgcg ttcactggaa atccctgccg cgggcttttg 120
 agagcacagt gctttcagca tcctctgggt cctttggatg gcgctgcagt cggagacatt 180
 gatcagagat tctagagctg cgcagtacat gccggcggtc aggttgacgc tccacaccat 240
 gctgccgttg cagaggggatg cctgattctg ggtgatgttg accagctcct caatgagctc 300
 cttgaggggtt ggggagggag tcacagggct cggggaggca aggccaccga ggcaggtgag 360
 agcaatgacc acagtcaacc agagcgccat 390

<210> 104
 <211> 330
 <212> DNA
 <213> Canis familiaris

<220>
 <221> CDS
 <222> (1)..(330)

<400> 104
 agc cct gtg act ccc tcc cca acc ctc aag gag ctc att gag gag ctg 48
 Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu Ile Glu Glu Leu
 1 5 10 15
 gtc aac atc acc cag aat cag gca tcc ctc tgc aac ggc agc atg gtg 96
 Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn Gly Ser Met Val
 20 25 30

tgg agc gtc aac ctg acc gcc ggc atg tac tgc gca gct cta gaa tct 144
 Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu Glu Ser
 35 40 45

ctg atc aat gtc tcc gac tgc agc gcc atc caa agg acc cag agg atg 192
 Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg Thr Gln Arg Met
 50 55 60

ctg aaa gca ctg tgc tct caa aag ccc gcg gca ggg att tcc agt gaa 240
 Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly Ile Ser Ser Glu
 65 70 75 80

cgc agc cga gac acc aaa att gaa gtg atc cag ttg gtg aaa aac ctg 288
 Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu Val Lys Asn Leu
 85 90 95

ctc acc tat gta agg gga gtt tat cgc cat gga aat ttc aga 330
 Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn Phe Arg
 100 105 110

<210> 105

<211> 110

<212> PRT

<213> Canis familiaris

<400> 105

Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu Ile Glu Glu Leu
 1 5 10 15

Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn Gly Ser Met Val
 20 25 30

Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu Glu Ser
 35 40 45

Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg Thr Gln Arg Met
 50 55 60

Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly Ile Ser Ser Glu
 65 70 75 80

Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu Val Lys Asn Leu
 85 90 95

Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn Phe Arg
 100 105 110

257

<210> 106
 <211> 330
 <212> DNA
 <213> Canis familiaris

<400> 106
 tctgaaat t t ccatggcgat aaactcccct tacataggtg agcaggtttt tcaccaactg 60
 gatcacttca attttgggtgt ctggtgtgctg ttcactggaa atccctgccg cgggcttttg 120
 agagcacagt gctttcagca tcctctgggt cctttggatg gcgctgcagt cggagacatt 180
 gatcagagat tctagagctg cgcagtacat gccggcgggtc aggttgacgc tccacaccat 240
 gctgccgttg cagaggggatg cctgattctg ggtgatgttg accagctcct caatgagctc 300
 cttgaggggtt ggggagggag tcacagggct 330

<210> 107
 <211> 567
 <212> DNA
 <213> Felis catus

<220>
 <221> CDS
 <222> (1)..(567)

<400> 107
 atg gcg ctg ccc tct tcc ttc ttg gtg gcc ctg gtg gcg ctg ggc tgc 48
 Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys
 1 5 10 15
 aac tcc gtc tgc tct ctg ggc tgt gac ctg cct cag acc cac ggc ctg 96
 Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu
 20 25 30
 ctg aac agg agg gcc ttg acg ctc ctg gga caa atg agg aga ctc cct 144
 Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro
 35 40 45
 gcc agc tcc tgt cag aag gac aga aat gac ttc gcc ttc ccc cag gac 192
 Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp
 50 55 60
 gtg ttt ggt gga gac cag tcc cac aag gcc caa gcc ctc tcg gtg gtg 240
 Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val

258

65	70	75	80	
cac gtg acg aac cag aag atc ttc cac ttc ttc tgc aca gag gcg tcc				288
His Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser.				
	85	90	95	
tcg tct gct gct tgg aac acc acc ctc ctg gag gaa ttc tgc acg gga				336
Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly				
	100	105	110	
ctt gat tgg cag ctg acc cgc ctg gaa gcc tgt gtc atg cag gag gtg				384
Leu Asp Trp Gln Leu Thr Arg Leu Glu Ala Cys Val Met Gln Glu Val				
	115	120	125	
ggg gag gga gag gct ccc ctc acg aac gag gac tcc atc ctg agg aac				432
Gly Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ser Ile Leu Arg Asn				
	130	135	140	
tac ttc caa aga ctc tcc ctc tac ctg caa gag aag aaa tac agc cct				480
Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro				
	145	150	155	160
tgt gcc tgg gag atc gtc aga gca gaa atc atg aga tcc ttg tat tat				528
Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr				
	165	170	175	
tca tca aca gcc ttg cag aaa aga tta agg agc gag aaa				567
Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys				
	180	185		
<210> 108				
<211> 189				
<212> PRT				
<213> Felis catus				
<400> 108				
Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys				
1	5	10	15	
Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu				
	20	25	30	
Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro				
	35	40	45	
Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp				
	50	55	60	

Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val
65 70 75 80

His Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser
85 90 95

Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly
100 105 110

Leu Asp Trp Gln Leu Thr Arg Leu Glu Ala Cys Val Met Gln Glu Val
115 120 125

Gly Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ser Ile Leu Arg Asn
130 135 140

Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro
145 150 155 160

Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr
165 170 175

Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys
180 185

<210> 109

<211> 567

<212> DNA

<213> Felis catus

<400> 109

tttctcgtc cttaatcttt tctgcaaggc tgttgatgaa taatacaagg atctcatgat 60

ttctgctctg acgatctccc aggcacaagg gctgtatttc ttctcttgca ggtagaggga 120

gagtctttgg aagtagttcc tcaggatgga gtcctcgttc gtgaggggag cctctccctc 180

ccccacctcc tgcattgacac aggtctccag gcgggtcagc tgccaatcaa gtcccgtgca 240

gaattcctcc aggagggtgg tgttccaagc agcagacgag gacgcctctg tgcagaagaa 300

gtggaagatc ttctggttcg tcacgtgcac caccgagagg gcttgggcct tgtgggactg 360

gtctccacca aacacgtcct gggggaaggc gaagtcattt ctgtccttct gacaggagct 420

ggcaggaggt ctctcattt gtcccaggag cgtcaaggcc ctctgttca gcaggccgtg 480

gggtctgagggc aggtcacagc ccagagagca gacggagttg cagcccagcg ccaccagggc 540

caccaagaag gaagagggca gcgccat 567

<210> 110

<211> 567

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (1)..(567)

<400> 110

atg gcg ctg ccc tct tcc ttc ttg gtg gcc ctg gtg gcg ctg ggc tgc 48
Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys
1 5 10 15

aac tcc gtc tgc tct ctg ggc tgt gac ctg cct cag acc cac ggc ctg 96
Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu
20 25 30

ctg aac agg agg gcc ttg acg ctc ctg gga caa atg agg aga ctc cct 144
Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro
35 40 45

gcc agc tcc tgt cag aag gac agg aat gac ttc gcc ttc ccc cag gac 192
Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp
50 55 60

gtg ttc ggt gga gac cag tcc cac aag gct caa gcc ctc tcg gtg gtg 240
Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val
65 70 75 80

cac gtg acg aac cag gag atc ttc cac ttc ttc tgc aca gag gcg tcc 288
His Val Thr Asn Gln Glu Ile Phe His Phe Phe Cys Thr Glu Ala Ser
85 90 95

tcg tct gct gct tgg aac acc acc ctc ctg gag gaa ttc tgc acg gga 336
Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly
100 105 110

ctt gat cgg cag ctg acc cgc ctg gaa gcc tgt gtc gtg cag gag gtg 384
Leu Asp Arg Gln Leu Thr Arg Leu Glu Ala Cys Val Val Gln Glu Val
115 120 125

ggg gag gga gag gct ccc ctc acg aac gag gac tcc ctc ctg agg aac 432

Gly Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ser Leu Leu Arg Asn
 130 135 140

tac ttc caa aga ctc tcc ctc tac ctg caa gag aag aaa tac agc cct 480
 Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro
 145 150 155 160

tgt gcc tgg gag atc gtc aga gca gaa atc atg aga tcc ttg tat tat 528
 Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr
 165 170 175

tca tca aca gcc ttg caa aaa aga tta agg agc gag aaa 567
 Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys
 180 185

<210> 111
 <211> 189
 <212> PRT
 <213> Felis catus

<400> 111
 Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys
 1 5 10 15

Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu
 20 25 30

Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro
 35 40 45

Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp
 50 55 60

Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val
 65 70 75 80

His Val Thr Asn Gln Glu Ile Phe His Phe Phe Cys Thr Glu Ala Ser
 85 90 95

Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly
 100 105 110

Leu Asp Arg Gln Leu Thr Arg Leu Glu Ala Cys Val Val Gln Glu Val
 115 120 125

Gly Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ser Leu Leu Arg Asn
 130 135 140

Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro
 145 150 155 160

Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr
 165 170 175

Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys
 180 185

<210> 112
 <211> 567
 <212> DNA
 <213> Felis catus

<400> 112
 tttctcgtc cttaatcttt ttgtcaaggc tgttgatgaa taatacaagg atctcatgat 60
 ttctgctctg acgatctccc aggcacaagg gctgtatttc ttctcttgca ggtagaggga 120
 gagtctttgg aagtagttcc tcaggaggga gtcctcggtc gtgaggggag cctctccctc 180
 cccacctcc tgcacgacac aggcttccag gcgggtcagc tgccgatcaa gtcccgtgca 240
 gaattcctcc aggaggggtg tgttccaagc agcagacgag gacgcctctg tgcagaagaa 300
 gtggaagatc tcctgggtcg tcacgtgcac caccgagagg gcttgagcct tgtgggactg 360
 gtctccaccg aacacgtcct gggggaaggc gaagtcattc ctgtccttct gacaggagct 420
 ggcagggagt ctctcattt gtcccaggag cgtcaaggcc ctctgttca gcaggccgtg 480
 ggtctgaggc aggtcacagc ccagagagca gacggagttg cagcccagcg ccaccagggc 540
 caccaagaag gaagagggca gcgcoat 567

<210> 113
 <211> 498
 <212> DNA
 <213> Felis catus

<220>
 <221> CDS
 <222> (1)..(498)

<400> 113

tgt gac ctg cct cag acc cac ggc ctg ctg aac agg agg gcc ttg acg	48
Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr	
1 5 10 15	
ctc ctg gga caa atg agg aga ctc cct gcc agc tcc tgt cag aag gac	96
Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp	
20 25 30	
aga aat gac ttc gcc ttc ccc cag gac gtg ttt ggt gga gac cag tcc	144
Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser	
35 40 45	
cac aag gcc caa gcc ctc tcg gtg gtg cac gtg acg aac cag aag atc	192
His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Lys Ile	
50 55 60	
ttc cac ttc ttc tgc aca gag gcg tcc tcg tct gct gct tgg aac acc	240
Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn Thr	
65 70 75 80	
acc ctc ctg gag gaa ttc tgc acg gga ctt gat tgg cag ctg acc cgc	288
Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Trp Gln Leu Thr Arg	
85 90 95	
ctg gaa gcc tgt gtc atg cag gag gtg ggg gag gga gag gct ccc ctc	336
Leu Glu Ala Cys Val Met Gln Glu Val Gly Glu Gly Glu Ala Pro Leu	
100 105 110	
acg aac gag gac tcc atc ctg agg aac tac ttc caa aga ctc tcc ctc	384
Thr Asn Glu Asp Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu	
115 120 125	
tac ctg caa gag aag aaa tac agc cct tgt gcc tgg gag atc gtc aga	432
Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg	
130 135 140	
gca gaa atc atg aga tcc ttg tat tat tca tca aca gcc ttg cag aaa	480
Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys	
145 150 155 160	
aga tta agg agc gag aaa	498
Arg Leu Arg Ser Glu Lys	
165	

<210> 114
 <211> 166
 <212> PRT

<213> Felis catus

<400> 114

Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr
1 5 10 15

Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp
20 25 30

Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser
35 40 45

His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Lys Ile
50 55 60

Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn Thr
65 70 75 80

Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Trp Gln Leu Thr Arg
85 90 95

Leu Glu Ala Cys Val Met Gln Glu Val Gly Glu Gly Glu Ala Pro Leu
100 105 110

Thr Asn Glu Asp Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu
115 120 125

Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg
130 135 140

Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys
145 150 155 160

Arg Leu Arg Ser Glu Lys
165

<210> 115

<211> 498

<212> DNA

<213> Felis catus

<400> 115

tttctcgcctc cttaatcttt tctgcaaggc tgttgatgaa taatacaagg atctcatgat 60

ttctgctctg acgatctccc aggcacaagg gctgtatttc ttctcttgca ggtagaggga 120

gagtctttgg aagtagttcc tcaggatgga gtcctcgttc gtgaggggag cctctccctc 180

265

cccacctcc tgcattgacac aggtttccag gcgggtcagc tgccaatcaa gtcccgtgca 240
 gaattcctcc aggaggggtgg tgttccaagc agcagacgag gacgcctctg tgcagaagaa 300
 gtggaagatc ttctggttcg tcacgtgcac caccgagagg gcttgggcct tgtgggactg 360
 gtctccacca aacacgtcct gggggaaggc gaagtcattt ctgtccttct gacaggagct 420
 ggcagggagt ctctcattt gtcccaggag cgtcaaggcc ctctgttca gcaggccgtg 480
 ggtctgaggc aggtcaca 498

<210> 116
 <211> 498
 <212> DNA
 <213> Felis catus

<220>
 <221> CDS
 <222> (1)..(498)

<400> 116
 tgt gac ctg cct cag acc cac ggc ctg ctg aac agg agg gcc ttg acg 48
 Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr
 1 5 10 15
 ctc ctg gga caa atg agg aga ctc cct gcc agc tcc tgt cag aag gac 96
 Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp
 20 25 30
 agg aat gac ttc gcc ttc ccc cag gac gtg ttc ggt gga gac cag tcc 144
 Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser
 35 40 45
 cac aag gct caa gcc ctc tcg gtg gtg cac gtg acg aac cag gag atc 192
 His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Glu Ile
 50 55 60
 ttc cac ttc ttc tgc aca gag gcg tcc tcg tct gct gct tgg aac acc 240
 Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn Thr
 65 70 75 80
 acc ctc ctg gag gaa ttc tgc acg gga ctt gat cgg cag ctg acc cgc 288
 Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln Leu Thr Arg
 85 90 95

206

ctg gaa gcc tgt gtc gtg cag gag gtg ggg gag gga gag gct ccc ctc 336
 Leu Glu Ala Cys Val Val Gln Glu Val Gly Glu Gly Glu Ala Pro Leu
 100 105 110

acg aac gag gac tcc ctc ctg agg aac tac ttc caa aga ctc tcc ctc 384
 Thr Asn Glu Asp Ser Leu Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu
 115 120 125

tac ctg caa gag aag aaa tac agc cct tgt gcc tgg gag atc gtc aga 432
 Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg
 130 135 140

gca gaa atc atg aga tcc ttg tat tat tca tca aca gcc ttg caa aaa 480
 Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys
 145 150 155 160

aga tta agg agc gag aaa 498
 Arg Leu Arg Ser Glu Lys
 165

<210> 117
 <211> 166
 <212> PRT
 <213> Felis catus

<400> 117
 Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr
 1 5 10 15

Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp
 20 25 30

Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser
 35 40 45

His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Glu Ile
 50 55 60

Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn Thr
 65 70 75 80

Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln Leu Thr Arg
 85 90 95

Leu Glu Ala Cys Val Val Gln Glu Val Gly Glu Gly Glu Ala Pro Leu
 100 105 110

267

CGTCT = 2631560

Thr Asn Glu Asp Ser Leu Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu
 115 120 125

Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg
 130 135 140

Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys
 145 150 155 160

Arg Leu Arg Ser Glu Lys
 165

<210> 118
 <211> 498
 <212> DNA
 <213> Felis catus

<400> 118
 tttctcgctc cttaatcttt ttgcaaggc tgttgatgaa taatacaagg atctcatgat 60
 ttctgctctg acgatctccc aggcacaagg gctgtatttc ttctcttgca ggtagaggga 120
 gagtctttgg aagtagttcc tcaggaggga gtcctcgttc gtgaggggag cctctccctc 180
 cccacctcc tgcacgacac aggcttccag gcgggtcagc tgccgatcaa gtcccgtgca 240
 gaattcctcc aggagggtgg tgttccaagc agcagacgag gacgcctctg tgcagaagaa 300
 gtggaagate tcctggttcg tcacgtgcac caccgagagg gcttgagcct tgtgggactg 360
 gtctccaccg aacacgtcct gggggaaggc gaagtcattc ctgtccttct gacaggagct 420
 ggcagggagt ctctcathtt gtcccaggag cgtcaaggcc ctctgttca gcaggccgtg 480
 ggtctgaggc aggtcaca 498

<210> 119
 <211> 444
 <212> DNA
 <213> Felis catus

<220>
 <221> CDS
 <222> (10)..(441)

<400> 119

Ser Ala Pro Thr Ser Ser Pro Ser Ser Val Thr Arg Pro Trp Gln His
20 25 30

Val Asp Ala Ile Lys Glu Ala Leu Ser Leu Leu Asn Asn Ser Ser Glu
35 40 45

Ile Thr Ala Val Met Asn Glu Ala Val Glu Val Val Ser Glu Met Phe
50 55 60

Asp Pro Glu Glu Pro Lys Cys Leu Gln Thr His Leu Lys Leu Tyr Glu
65 70 75 80

Gln Gly Leu Arg Gly Ser Leu Ile Ser Leu Lys Glu Pro Leu Arg Met
85 90 95

Met Ala Asn His Tyr Lys Gln His Cys Pro Leu Thr Pro Glu Thr Pro
100 105 110

Cys Glu Thr Gln Thr Ile Thr Phe Lys Asn Phe Lys Glu Asn Leu Lys
115 120 125

Asp Phe Leu Phe Asn Asn Pro Phe Asp Cys Trp Gly Pro Asp Gln Lys
130 135 140

<210> 121

<211> 444

<212> DNA

<213> Felis catus

<400> 121

ttactttctgg tctggtcccc agcagtc aaa ggggttgta aacagaaaat ccttcagatt 60

ctctttgaaa tttttgaagg tgatagtctg ggtttcacag ggcgtttccg gagtaagggg 120

gcagtgtctgc ttgtaatggt tggccatcat tctcagaggc tccttgaggc tgatgaggct 180

gccccgtagg cctgtctcgt acagcttttag gtgagtctgc aggcatttcg gctcctcagg 240

gtcaaacatt tcagagacga cttctactgc ttcattcatc acagcagtta tttcactact 300

gttgttcaga aggctcaggg cctccttgat ggcattccacg tggttgccagg gccgagtgc 360

agagctgggt gaactggtgg gtgcagagat gctgcagacc acagtgccca ggaaaagcag 420

gttctgcagc cacatggtgg atcc 444

<210> 122
<211> 432
<212> DNA
<213> Felis catus

<400> 122
atgtggctgc agaacctgct tttcctgggc actgtggtct gcagcatctc tgcacccacc 60
agttcaccca gctctgtcac tcggccctgg caacacgtgg atgccatcaa ggaggccctg 120
agccttctga acaacagtag tgaaataact gctgtgatga atgaagcagt agaagtcgtc 180
tctgaaatgt ttgacctga ggagccgaaa tgcctgcaga ctcacctaaa gctgtacgag 240
cagggcctac ggggcagcct catcagcctc aaggagcctc tgagaatgat ggccaaccat 300
tacaagcagc actgccccct tactccgga acgccctgtg aaaccagac tatcaccttc 360
aaaaatttca aagagaatct gaaggatttt ctgtttaaca acccctttga ctgctgggga 420
ccagaccaga ag 432

<210> 123
<211> 432
<212> DNA
<213> Felis catus

<400> 123
cttctggtct ggtccccagc agtcaaaggg gttgttaa ac agaaaatcct tcagattctc 60
tttgaaattt ttgaagggtga tagtctgggt ttacagggc gtttccggag taagggggca 120
gtgctgcttg taatgggttg ccatcattct cagaggctcc ttgaggctga tgaggctgcc 180
ccgtaggccc tgctcgtaca gctttaggtg agtctgcagg catttcggct cctcagggtc 240
aacatttca gagacgactt ctactgcttc attcatcaca gcagttattt cactactgtt 300
gttcagaagg ctcagggcct ccttgatggc atccacgtgt tgccagggcc gagtgacaga 360
gctgggtgaa ctggtgggtg cagagatgct gcagaccaca gtgccagga aaagcaggtt 420
ctgcagccac at 432

<210> 124

<211> 381
 <212> DNA
 <213> Felis catus

<220>
 <221> CDS
 <222> (1)..(381)

<400> 124

gca ccc acc agt tca ccc agc tct gtc act cgg ccc tgg caa cac gtg 48
 Ala Pro Thr Ser Ser Pro Ser Ser Val Thr Arg Pro Trp Gln His Val
 1 5 10 15

gat gcc atc aag gag gcc ctg agc ctt ctg aac aac agt agt gaa ata 96
 Asp Ala Ile Lys Glu Ala Leu Ser Leu Leu Asn Asn Ser Ser Glu Ile
 20 25 30

act gct gtg atg aat gaa gca gta gaa gtc gtc tct gaa atg ttt gac 144
 Thr Ala Val Met Asn Glu Ala Val Glu Val Val Ser Glu Met Phe Asp
 35 40 45

cct gag gag ccg aaa tgc ctg cag act cac cta aag ctg tac gag cag 192
 Pro Glu Glu Pro Lys Cys Leu Gln Thr His Leu Lys Leu Tyr Glu Gln
 50 55 60

ggc cta cgg ggc agc ctc atc agc ctc aag gag cct ctg aga atg atg 240
 Gly Leu Arg Gly Ser Leu Ile Ser Leu Lys Glu Pro Leu Arg Met Met
 65 70 75 80

gcc aac cat tac aag cag cac tgc ccc ctt act ccg gaa acg ccc tgt 288
 Ala Asn His Tyr Lys Gln His Cys Pro Leu Thr Pro Glu Thr Pro Cys
 85 90 95

gaa acc cag act atc acc ttc aaa aat ttc aaa gag aat ctg aag gat 336
 Glu Thr Gln Thr Ile Thr Phe Lys Asn Phe Lys Glu Asn Leu Lys Asp
 100 105 110

ttt ctg ttt aac aac ccc ttt gac tgc tgg gga cca gac cag aag 381
 Phe Leu Phe Asn Asn Pro Phe Asp Cys Trp Gly Pro Asp Gln Lys
 115 120 125

<210> 125
 <211> 127
 <212> PRT
 <213> Felis catus

<400> 125

Ala Pro Thr Ser Ser Pro Ser Ser Val Thr Arg Pro Trp Gln His Val
 1 5 10 15

Asp Ala Ile Lys Glu Ala Leu Ser Leu Leu Asn Asn Ser Ser Glu Ile
 20 25 30

Thr Ala Val Met Asn Glu Ala Val Glu Val Val Ser Glu Met Phe Asp
 35 40 45

Pro Glu Glu Pro Lys Cys Leu Gln Thr His Leu Lys Leu Tyr Glu Gln
 50 55 60

Gly Leu Arg Gly Ser Leu Ile Ser Leu Lys Glu Pro Leu Arg Met Met
 65 70 75 80

Ala Asn His Tyr Lys Gln His Cys Pro Leu Thr Pro Glu Thr Pro Cys
 85 90 95

Glu Thr Gln Thr Ile Thr Phe Lys Asn Phe Lys Glu Asn Leu Lys Asp
 100 105 110

Phe Leu Phe Asn Asn Pro Phe Asp Cys Trp Gly Pro Asp Gln Lys
 115 120 125

<210> 126
 <211> 381
 <212> DNA
 <213> Felis catus

<400> 126
 cttctggtct ggtccccagc agtcaaagg gttgttaa ac agaaaatcct tcagattctc 60
 tttgaaat tttgaagg tga tagtctgggt ttcacagggc gtttccggag taagggggca 120
 gtgctgcttg taatgggttg ccatcattct cagaggctcc ttgaggctga tgaggctgcc 180
 ccgtaggccc tgctcgtaca gctttagggtg agtctgcagg catttcggct cctcagggtc 240
 aaacatttca gagacgactt ctactgcttc attcatcaca gcagttat ttt cactactgtt 300
 gttcagaagg ctcagggcct ccttgatggc atccacgtgt tgccagggcc gagtgacaga 360
 gctgggtgaa ctggtgggtg c 381

<210> 127
 <211> 28

<212> DNA

<213> Artificial Sequence

<400> 127

cctcgagatt cagctttcaa tgcctgta

28

<210> 128

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 128

tgcccrstcg gcttcttctc c

21

<210> 129

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 129

cgactctctt tccctctctc ctg

23

<210> 130

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 130

cctcaaattg cggcacatgt c

21

<210> 131

<211> 22

<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 131
ctgttcagag tttgagtaag cc

22

<210> 132

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 132
gaagatacca tttcaacttt aacacagc

28

<210> 133

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 133
tgctgtattg tgaagactcc cagc

24

<210> 134

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 134
atgcactttc tttgcc

16

<210> 135
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 135
ctggaggaaa akacttcrat gattctgata tctgaaatat at

42

<210> 136
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 136
ctgacycttk sttggscttc attctca

27

<210> 137
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 137
gggctcgaga aaagatttgc tgtagaaaat cccatg

36

<210> 138
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Primer

<400> 138
cccgcggccg ctcaactttc cgggtgtccac tc 32

<210> 139
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 139
gtcmtggctc tyrcttgcoct tgg 23

<210> 140
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 140
aaastgggcy acytcgattt tgg 23

<210> 141
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 141
gtgatgttgm ycagctcctc 20

<210> 142
<211> 20
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 142

aattaaccct cactaaaggg

20

<210> 143

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 143

atggcgctct gggtgactgt

20

<210> 144

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 144

ggcttttgag agcacagtgc

20

<210> 145

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 145

ccccatatga gccctgtgac tccctcccc

29

<210> 146
<211> 30
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 146
ggggaattct catctgaaat ttccatggcg

30

<210> 147
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 147
atggcgctgc cctcttcctt cttg

24

<210> 148
<211> 28
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 148
tcatttctcg ctccttaatc ttttctgc

28

<210> 149
<211> 37
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 149
cagggatcca ccatgtggct gcagaacctg cttttcc

37

<210> 150
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 150
ttacttctgg tctggtcccc agcagtcaaa ggggttgta aacagaaaat

50

<210> 151
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 151
cacagyccca tctcctcc

18

<210> 152
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 152
gtaatacgac tcactatagg gc

22

<210> 153
<211> 26
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 153

acggaattcg agatgatagt gctggc

26

<210> 154

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 154

gtgtctagat ttggtagaaa aggatgat

28

<210> 155

<211> 567

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (1)..(567)

<400> 155

atg gcg ctg ccc tct tcc ttc ttg gtg gcc ctg gtg gcg ctg ggc tgc 48
Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys
1 5 10 15

aac tcc gtc tgc tct ctg ggc tgt gac ctg cct cag acc cac ggc ctg 96
Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu
20 25 30

ctg aac agg agg gcc ttg acg ctc ctg gga caa atg agg aga ctc cct 144
Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro
35 40 45

gcc agc tcc tgt cag aag gac aga agt gac ttc gcc ttc ccc cag gac 192
Ala Ser Ser Cys Gln Lys Asp Arg Ser Asp Phe Ala Phe Pro Gln Asp
50 55 60

ggcagggagt ctctcatatt gtcccaggag cgtcaaggcc ctctgttca gcaggccgtg 480
 ggtctgaggc aggtcacagc ccagagagca gacggagttg cagcccagcg ccaccagggc 540
 caccaagaag gaagagggca gcgccat 567

<210> 158
 <211> 498
 <212> DNA
 <213> Felis catus

<220>
 <221> CDS
 <222> (1)..(498)

<400> 158
 tgt gac ctg cct cag acc cac ggc ctg ctg aac agg agg gcc ttg acg 48
 Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr
 1 5 10 15
 ctc ctg gga caa atg agg aga ctc cct gcc agc tcc tgt cag aag gac 96
 Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp
 20 25 30
 aga agt gac ttc gcc ttc ccc cag gac gtg ttt ggt gga gac cag tcc 144
 Arg Ser Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser
 35 40 45
 cac aag gcc caa gcc ctc tcg gtg gtg cac gtg acg aac cag aag atc 192
 His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Lys Ile
 50 55 60
 ttc cac ttc ttc tgc aca gag gcg tcc tcg tct gct gct tgg aac acc 240
 Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn Thr
 65 70 75 80
 acc ctc ctg gag gaa ttc tgc acg gga ctt gat tgg cag ctg acc cgc 288
 Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Trp Gln Leu Thr Arg
 85 90 95
 ctg gaa gcc tgt gtc atg cag gag gtg ggg gag gga gag gct ccc ctc 336
 Leu Glu Ala Cys Val Met Gln Glu Val Gly Glu Gly Glu Ala Pro Leu
 100 105 110
 acg aac gag gac tcc atc ctg agg aac tac ttc caa aga ctc tcc ctc 384
 Thr Asn Glu Asp Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu
 115 120 125

145

150

155

160

Arg Leu Arg Ser Glu Lys
165

<210> 160

<211> 498

<212> DNA

<213> Felis catus

<400> 160

tttctcgctc cttaatcttt tctgcaaggc tgttgatgaa taatacaagg atctcatgat 60

ttctgctctg acgatctccc aggcacaagg gctgtatttc ttctcttgca ggtagaggga 120

gagtctttgg aagtagttcc tcaggatgga gtccctcggtc gtgaggggag cctctccctc 180

ccccacctcc tgcattgacac aggtctccag gcgggtcagc tgccaatcaa gtcccgtgca 240

gaattcctcc aggaggggtgg tgttccaagc agcagacgag gacgcctctg tgcagaagaa 300

gtggaagatc ttctgggttcg tcacgtgcac caccgagagg gcttgggcct tgtgggactg 360

gtctccacca aacacgtcct gggggaaggc gaagtcactt ctgtccttct gacaggagct 420

ggcagggagt ctctcattt gtcccaggag cgtcaaggcc ctctgttca gcaggccgtg 480

ggtctgaggc aggtcaca 498

<210> 161

<211> 582

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (1)..(582)

<400> 161

atg gcg ctg ccc tct tcc ttc ttg gtg gcc ctg gtg gcg ctg ggc tgc 48

Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys

1

5

10

15

aac tcc gtc tgc tct ctg ggc tgt gat ctg cct cag acc cac ggc ctg 96

Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu

20

25

30

<213> Felis catus

<400> 162

Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys
1 5 10 15

Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu
20 25 30

Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro
35 40 45

Ala Ser Ser Cys Gln Lys Asp Arg Ser Asp Phe Ala Phe Pro Gln Asp
50 55 60

Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val
65 70 75 80

His Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser
85 90 95

Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly
100 105 110

Leu Asp Arg Gln Leu Thr Arg Leu Glu Ala Cys Val Val Gln Glu Val
115 120 125

Gly Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ile His Pro Glu Asp
130 135 140

Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu
145 150 155 160

Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met
165 170 175

Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser
180 185 190

Glu Lys

<210> 163

<211> 582

<212> DNA

<213> Felis catus

<400> 163

tttctcgctc cttaatcttt tctgcaaggc tgttgatgaa taatacaagg atctcatgat 60
 ttctgctctg acgatctccc aggcacaagg gctgtatttc ttctcttgca ggtagaggga 120
 gagtctttgg aagtagttcc tcaggatgga gtcctcgga tgaatgtcct cgttcgtcag 180
 gggagcctct cctccccca cctcctgcac gacacaggct tccaggcggg tcagctgccg 240
 atcaagtccc gtgcagaatt cctccaggag ggtggtgttc caagcagcag acgaggacgc 300
 ctctgtgcag aagaagtgga agatcttctg gttcgtcacg tgcaccaccg agagggttg 360
 ggccttggtg gactggtctc caccgaacac gtcctggggg aaggcgaagt cacttctgtc 420
 cttctgacag gagctggcag ggagtctcct catttgctcc aggagcgtca aggccctcct 480
 gttcagcagg ccgtgggtct gaggcagatc acagcccaga gagcagacgg agttgcagcc 540
 cagcgccacc agggccacca agaaggaaga gggcagcgcc at 582

<210> 164

<211> 513

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (1)..(513)

<400> 164

tgt gat ctg cct cag acc cac ggc ctg ctg aac agg agg gcc ttg acg 48
 Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr
 1 5 10 15
 ctc ctg gga caa atg agg aga ctc cct gcc agc tcc tgt cag aag gac 96
 Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp
 20 25 30
 aga agt gac ttc gcc ttc ccc cag gac gtg ttc ggt gga gac cag tcc 144
 Arg Ser Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser
 35 40 45
 cac aag gcc caa gcc ctc tcg gtg gtg cac gtg acg aac cag aag atc 192
 His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Lys Ile
 50 55 60

ttc cac ttc ttc tgc aca gag gcg tcc tcg tct gct gct tgg aac acc 240
Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn Thr
65 70 75 80

acc ctc ctg gag gaa ttc tgc acg gga ctt gat cgg cag ctg acc cgc 288
Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln Leu Thr Arg
85 90 95

ctg gaa gcc tgt gtc gtg cag gag gtg ggg gag gga gag gct ccc ctg 336
Leu Glu Ala Cys Val Val Gln Glu Val Gly Glu Gly Glu Ala Pro Leu
100 105 110

acg aac gag gac att cat ccc gag gac tcc atc ctg agg aac tac ttc 384
Thr Asn Glu Asp Ile His Pro Glu Asp Ser Ile Leu Arg Asn Tyr Phe
115 120 125

caa aga ctc tcc ctc tac ctg caa gag aag aaa tac agc cct tgt gcc 432
Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala
130 135 140

tgg gag atc gtc aga gca gaa atc atg aga tcc ttg tat tat tca tca 480
Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser
145 150 155 160

aca gcc ttg cag aaa aga tta agg agc gag aaa 513
Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys
165 170

<210> 165
<211> 171
<212> PRT
<213> Felis catus

<400> 165
Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr
1 5 10 15

Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp
20 25 30

Arg Ser Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser
35 40 45

His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Lys Ile
50 55 60

Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn Thr

80

Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys
165 170

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<210> 166
<211> 513
<212> DNA
<213> Felis catus
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<400> 166
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ttctgctctg acgatctccc aggcacaagg gctgtatttc ttctcttgca ggtagaggga 120
gagtctttgg aagtagttcc tcaggatgga gtcctcgggg tgaatgtcct cgttcgtcag 180
gggagcctct ccctcccca cctcctgcac gacacaggct tccaggcggg tcagctgccg 240
atcaagtccc gtgcagaatt cctccaggag ggtggtgttc caagcagcag acgaggacgc 300
ctctgtgcag aagaagtgga agatcttctg gttcgtcacg tgcaccaccg agagggcttg 360
ggccttgtgg gactggtctc caccgaacac gtctggggg aaggcgaagt cacttctgtc 420
cttctgacag gagctggcag ggagtctcct catttgtccc aggagcgtca aggcctcct 480
gttcagcagg ccgtgggtct gaggcagatc aca 513
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$$\begin{array}{ll} \langle 210 \rangle & 167 \\ \langle 211 \rangle & 567 \end{array}$$

291

<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (1)..(567)

<400> 167

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Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys	
1 5 10 15	
aac tct gtc tgc tct ctg ggc tgt gac ctg cct cag acc cac ggc ctg	96
Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu	
20 25 30	
ctg aac agg agg gcc ttg acg ctc ctg gga caa atg agg aga ctc cct	144
Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro	
35 40 45	
gcc agc tcc tgc cag aag gac aga aat gac ttc gcc ttc ccc cag gac	192
Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp	
50 55 60	
gtg ttc ggt gga gac cag tcc cac aag gcc caa gcc ctc tcg gtg gtg	240
Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val	
65 70 75 80	
cac gtg acg aac cag aag atc ttc cac ttc ttc tgc aca gag gcg tcc	288
His Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser	
85 90 95	
tcg tct gct gct tgg aac acc acc ctc ctg gag gaa ttc tgc acg gga	336
Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly	
100 105 110	
ctt gat cgg cag ctg acc cgc ctg gaa gcc tgt gtc gtg cag gag gtg	384
Leu Asp Arg Gln Leu Thr Arg Leu Glu Ala Cys Val Val Gln Glu Val	
115 120 125	
ggg gag gga gag gct ccc ctc acg aac gag gac tcc atc ctg agg aac	432
Gly Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ser Ile Leu Arg Asn	
130 135 140	
tac ttc caa aga ctc tcc ctc tac ctg caa gag aag aaa tac agc cct	480
Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro	
145 150 155 160	

tgt gcc tgg gag atc gtc aga gca gaa atc atg aga tcc ttg tat tat 528
 Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr
 165 170 175

tca tca aca gcc ttg cag aaa aga tta agg agc gag aaa 567
 Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys
 180 185

<210> 168
 <211> 189
 <212> PRT
 <213> Felis catus

<400> 168
 Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys
 1 5 10 15

Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu
 20 25 30

Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro
 35 40 45

Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp
 50 55 60

Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val
 65 70 75 80

His Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser
 85 90 95

Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly
 100 105 110

Leu Asp Arg Gln Leu Thr Arg Leu Glu Ala Cys Val Val Gln Glu Val
 115 120 125

Gly Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ser Ile Leu Arg Asn
 130 135 140

Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro
 145 150 155 160

Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr
 165 170 175

293

66066T = 434360

Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys
 180 185

<210> 169
 <211> 567
 <212> DNA
 <213> Felis catus

<400> 169
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 gagtcttttg aagtagttcc tcaggatgga gtcctcgttc gtgaggggag cctctccctc 180
 cccacactcc tgcacgacac aggcttccag gcgggtcagc tgccgatcaa gtcccgtgca 240
 gaattcctcc aggaggggtg tgttccaagc agcagacgag gacgcctctg tgcagaagaa 300
 gtggaagatc ttctgggttcg tcacgtgcac caccgagagg gcttgggcct tgtgggactg 360
 gtctccaccg aacacgtcct gggggaaggc gaagtcattt ctgtccttct ggcaggagct 420
 ggcagggagt ctctcattt gtcccaggag cgtcaaggcc ctctgttca gcaggccgtg 480
 ggtctgaggc aggtcacagc ccagagagca gacagagttg cagcccagcg ccaccagggc 540
 caccaagaag gaagagggca gcgccat 567

<210> 170
 <211> 498
 <212> DNA
 <213> Felis catus

<220>
 <221> CDS
 <222> (1)..(498)

<400> 170
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 Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr
 1 5 10 15
 ctc ctg gga caa atg agg aga ctc cct gcc agc tcc tgc cag aag gac 96
 Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp
 20 25 30

294

20

25

30

Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser
 35 40 45

His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Lys Ile
 50 55 60

Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn Thr
 65 70 75 80

Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln Leu Thr Arg
 85 90 95

Leu Glu Ala Cys Val Val Gln Glu Val Gly Glu Gly Glu Ala Pro Leu
 100 105 110

Thr Asn Glu Asp Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu
 115 120 125

Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg
 130 135 140

Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys
 145 150 155 160

Arg Leu Arg Ser Glu Lys
 165

<210> 172

<211> 498

<212> DNA

<213> Felis catus

<400> 172

tttctcgctc cttaatcttt tctgcaaggc tgttgatgaa taatacaagg atctcatgat 60

ttctgctctg acgatctccc aggcacaagg gctgtatttc ttctcttgca ggtagaggga 120

gagtctttgg aagtagttcc tcaggatgga gtcctcgttc gtgaggggag cctctccctc 180

ccccacctcc tgcacgacac aggcttccag gcgggtcagc tgccgatcaa gtcccgtgca 240

gaattcctcc aggagggtgg tgttccaagc agcagacgag gacgcctctg tgcagaagaa 300

gtggaagatc ttctgggttcg tcacgtgcac caccgagagg gcttgggcct tgtgggactg 360

gtctccaccg aacacgtcct gggggaaggc gaagtcattt ctgtccttct ggcaggagct 420
ggcagggagt ctcttcattt gtcccaggag cgtcaaggcc ctctgttca gcaggccgtg 480
ggtctgaggc aggtcaca 498

<210> 173

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 173

attagatcc atggcgctgc cctcttct

29

<210> 174

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 174

gcctctagac tgtcatttct cgctccttaa tcttttctgc

40